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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                     Result
No.
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                     Score
544
523.5
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523
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655
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Gapop 10.0 , Gapext 0.5
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84.3
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                                                                                                                                                                                                                                                              Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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  123
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                                                                                               AAR81323
AAR81333
AAW22428
AAW22413
AAR81330
AAR81327
                     AAB30693
AAR76681
                                                                                AAW22410
                                                               AAW44124
                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                            Humanized VLA-4 an
Human VLA-4 reshap
Humanised alpha-4
Humanised alpha-4
                                                                                                                                                                                                                                               Description
      Chimaeric human/mu
                                            Heavy chain variab
A fusion of single
                                                                                    Alpha-4 integrin m
                                                                                                     Mouse anti-VLA-4 a Mouse VLA-4 antibo
                           Human/murine chime
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		21	139	74.0	484.5
ni gratable	AAWZ9/33	Τ	139	4	484.5
י מסוויל		14	139	74.0	484.5
-	•	15	143	4.	486
Heav	AAW21847	18	140	4	486
P 2 2 2	AAB74976	22	119	74.4	487
1 2	AAB74973	22	119	74.4	487
ALA	AAY52715	20	119	74.4	487
ATA	AAY52712	20	119	74.4	487
ישט-נ	AAR47491	15	120		487.5
	AAB74981	22	119		489
3 7 7	AAY52720	20	119	74.7	489
neavy c	AAW27551	18	120		489.5
C AIR-	AAB74969	22	119	75.0	491
AL 27 - C	AAY52708	20	119	75.0	491
10001	AAR57481	15	136		492
7700	AAR92079	17	117	5	492
ורפת שוורד	AAR57476	15	117	5	492
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	AAB74979	22	119	5	493
Humanised Air on	AAY52718	20	119	75.3	493
t	AAR81331	16	119	5	495
Humanised antibody	AAR92084	17	136	5	496
	AAB74980	22	119		499
ATX-0	AAY52719	20	119		499
ATK-U	AAB74978	22	119	76.8	503
ATR-0	AAY52717	20	119		
H CHAIL	AAR37611	14	118	7	504.5
nain var	AAB07969	21	135	. 7	
	AAW22425	18	119		512
	AAR81324	16	119	8	512
arpud	AAW22426	18	119	8	515
	AAR81325	16	119	8	515
numan/	AAW04397	17	269	79.8	523
	AAR76682	16	269	9	523

## ALIGNMENTS

AAR81323 RESULT

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AAR81323 standard; Protein; 123 AA

AAR81323;

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Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                                                                                                                                                                                                                                       Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                 02-APR-1996 (first entry)
                                                                                                                                                                 27-JUL-1995
                                                                                                                                                                                        W09519790-A1
                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                              antibody engineering.
Claim 11; Page 69; 105pp; English
                                                                                                                          25-JAN-1994;
                                                                                                                                               25-JAN-1995;
                            New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                             WPI; 1995-269276/35.
                                                                                Bendig MM, Jones TS,
                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC.
                  inflammatory disease.
                                                                                                                           94US-0186269.
                                                                                                                                                 95WO-US01219
                                                                                   Leger OJ, Saldanha J;
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RESULT
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Best Local
                         Region
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                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                          Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                            antibody engineering.
                                                                                                                                                                                                                                                                                                 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                              23-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               AAR81333;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR81333 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AA099889 and AA099892) regions are linked to human constant regions in the construction of a humanized modified using PCR primers (See AA099895-98) and then subcloned into constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the humanized light chain, amino acids L45, by the amino acid present in the equivalent position of the mouse by the amino acid present in the equivalent position of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating inflammatory diseases such as multiple sclerosis. can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-idiotype antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitis or encephalitis.
detecting VLA-4, for affini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 vss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA;
                                                    /note=
118..13
                                                                                                                                      /note=
55..68
                                                                                                                                                                 /note=
50..54
                          /note= "complementarity determining region 3"
132..142
                                                                                            /note=
                                                                                                                   /note= "framework region 2"
                                                                                                                                                                                                     /note= "signal peptide"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for affinity purification or for generating
                                                    . 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 655; DB 1 100.0%; Pred. No. 4e-53;
                                                           "framework region 3"
                                                                                  "complementarity determining region
     "framework region 4"
                                                                                                                                         "complementarity determining region
                                                                                                                                                                          "framework region 1"
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                                                                                                                                                                                                           AAW22428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                      Humanised alpha-4 integrin antibody 21.6 VL version Ha
                                                                                                              09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNAs are modified using PCR primers (AAQ)9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent chimeric antibodies are transfected into COS cells. The humanized antibodies are transfected into COS cells. The humanized endothelial cell and to treat inflammatory diseases such as multiple cerebral traumas, meningitis or encephalitis. The antibodies can be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                     AAW22428;
                                                                                                                                                                                 AAW22428 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5 and 3 ends of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                           140 vss 142
                                                                                                                                                                                                                                                                                                            121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09519790-A1
                                                                                                                                                                                                                                                                                                                                               61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                 20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                 \tt dpkfqgrvtitadtsastaymelsslrsedtavyy caregyygnygvyamdywgqgtlvt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 655; DB 16; 100.0%; Pred. No. 4.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Chimeric
Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric synthetic.
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         mutagenesis of appropriate mouse and human DNA sequences. The mutagenesis of appropriate mouse and human DNA sequences. The the sequences of appropriate mouse 21.6 VL (see AAW2242) can be used humanised 21.6 that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                      This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22413). It is composed of complementarity determining regions from the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28/CL framework. It can be expressed in mammalian host cells following PCR amplification and expressed in mammalian host cells following PCR amplification.
                                                                                                                                                                                                                                                                                                     Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT74789
                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                          (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-1997
                                                                                                                                                                                                                                                                                         asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                              Example 6; Fig 11; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO
                                                                                                                                                                                                                                                                                                                                                                                 Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Mat_protein /note= "VH version Ha (Claim 25)" 20..49
                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0561521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US18807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "21/28'CL framework region 1" 50..55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR2
/note= "21.6 complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= FR3
/note= "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "21.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 131
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                                                                                                                                                                                                                                                                                                                                                                                 Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                    Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                       Yednock TA;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised alpha-4 integrin antibody 21.6 VH Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW22413 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1997
                                                                                                                                                                                                                                                                                               /note= "21/28'CL framework region 1" Misc-difference 27..30
                                                                                                                                                                                                                                                                                                                                                                      Chimeric
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 vss 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VSS 123
                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                      Misc-difference 72
                                                                                                                                                       Region
WO9718838-A1
                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                          /note= "21/28'CL residues 27-30 are replaced by
                                             /label= CDR3 /note= "21.6 complementarity determining region 3" 113...123
                                                                                                                                                                                                                                   note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                /label= CDR1
                                  /label=
                                                                                                             /note= "21/28'CL
                                                                                                                                  /note= "21/28'CL framework region 3"
                                                                                                                                               /label= FR3
                                                                                                                                                                   /label= CDR2
/note= "21.6 complementarity determining region
                                                                                                                                                                                                     /note= "21/28'CL framework region
                                                                                                                                                                                                                  /label= FR2
                       /note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 655; DB 18; 100.0%; Pred. No. 4.7e-53;
                                                                                                                                                                                                                                                                      binding"
                                                                                                                                                                                                                                                                                 those of MAb
                                       FR4
                                                                                          loop"
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                                                                                                  VĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                    Arg-72 is substd. by Ala of mouse important in supporting the CDR2
                                                                                                                                                                                                                                                                                    21.6, involved in antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT
AAR81330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
            Mùs musculus
                                   antibody engineering.
                                        Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                        Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                                                                                                        AAR81330 standard; Protein; 123 AA
                                                                                                              02-APR-1996 (first entry)
                                                                                                                                                 AAR81330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28/CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of naturally occurring human antibodies.
                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Fig 7; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                   61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyandywgqgtlvt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                              1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                         vss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0561521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 648; DB 18;
Pred. No. 1.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yednock TA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids 145, 149, acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into cost. The humanized antibodies can be used to inhibit adhesion of a smultiple sclerosis. They can also be used in the treatment of stroke, used for detecting VLA-4, for affinity purification or for generating humanized antibodies.
Sequence
                                                                                                                                                                                             The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and
                                                                                                                                                                                                                                                                    Disclosure; Page 68; 105pp; English.
                                                                                                                                                                                                                                                                                                  inflammatory disease.
                                                                                                                                                                                                                                                                                                                   New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-269276/35
                                                                                                                                                                                                                                                                                                                                                                                Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09519790-A1
                                                                                                                                                                                                                                                                                                       leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "mouse heavy chain variable framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR3
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    region 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                           Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mouse heavy light chain variable framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining region
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                                                                                                                                                                                                                                                                                                                                                                           Saldanha J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR81327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR81327 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                              25-JAN-1994;
                                                                                                                                                                                                  25-JAN-1995;
                                                                                                                                                                                                                      27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
                                                                      New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                        Disclosure; Fig 2; 105pp; English.
                                                                                                     N-PSDB; AAQ99892
                                                                                                                 WPI; 1995-269276/35.
                                                                                                                                     Bendig MM,
                                                                                                                                                        (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewlgridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWWGRIDPANGYTKY 60
                                                               inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                        Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                               94US-0186269
                                                                                                                                                                                                     95WO-US01219.
                                                                                                                                                                                                                                                                                                                                                             /note=
55..68
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                                                   note= "complementarity determining region
                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%;
                                                                                                                                                                                                                                                                                                  . . 131
                                                                                                                                                                                                                                                                                                          "framework region 3"
                                                                                                                                                                                                                                                                                                                              "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                 "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                           "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                               "signal peptide"
                                                                                                                                       Leger OJ,
                                                                                                                                                                                                                                                                 "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-43;
[1; Mismatches 10
                                                                                                                                          Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                               for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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CC antibody against VIA-4. The 5' and 3' ends of the mouse cDNAs are commodified using PCR primers (See AAQ9995-98) and then subcloned into CC mammalian cell expression vectors containing human kappa or gamma-1 C constant regions. In the humanized heavy chain, amino acids H27, CC constant regions. In the humanized heavy chain, amino acids H27, CC constant regions. In the humanized heavy chain, amino acids H27, CC to the amino acid present in the equivalent position of the mouse C21. If y H chain. Plasmids encoding the chimteric antibodies are C21. If y H chain. Plasmids encoding the chimteric antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and CC to treat inflammatory diseases such as multiple sclerosis. They C can also be used in the treatment of stroke, cerebral traumas, C meningitis or encephalitis. The antibodies can also be used for affinity purification or for generating cantilogicus antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                               asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatorid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW22410 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 V 121
                                                                                                                                                                                                                                                       Region
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                                                                                                                                           Region
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                           Peptide
                                 Region
                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewlgridpangytky 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                      /note= "framework region 1"
50..54
                                                                                                                                                                                                                                                                             /label= Leader
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                       /label= FR1
/note= "framework region 3"
                                                                                                            /note= "framework region 2"
                                                                                                                                                                   /note
                                                                                                                                                                                    /label=
                                                         /note= "complementarity determining region
                                                                      /label= CDR2
                                                                                                                             /label= FR2
                 /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.1%; Score 544; DB 16; 82.6%; Pred. No. 7.5e-43;
                                                                                                                                                                 "complementarity determining region 1"
                                                                                                                                                                                        CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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This polypeptide comprises the heavy chain variable region (VH) of C mouse anti-alpha-4 integrin monoclonal antibody 21.6. The CC complementarity determining regions (CDRs) of the 21.6 VH can be CC incorporated into a human 21/28/CL framework to produce a claimed CC antibody that is used in the manufacture of a medicament for CC dementia, diabetes, inflammatory bowel disease, rheumatoid CC arthritis, transplant rejection, graft versus host disease, tumour CC ischaemia, and acute leukocyte mediated lung injury. The antibody CC may also be used in the affinity purification of alpha-4 integrin CC generating idiotypic antibodies. The humanised antibodies of the convertion have a half-life in the human circulation essentially convircing human antibodies of the convertion have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
           Heavy chain variable region of humanised NR-LU-13 antibody NRX451
                                                       05-JUN-1998 .(first entry)
                                                                                                  AAW44124;
                                                                                                                          AAW44124 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                        140 v 140
                                                                                                                                                                                                                                                           121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 69-70; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT74760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09718838-A1
                                                                                                                                                                                                                                                                          80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC
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                                                                                                                                                                                                                                                                                             61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                             20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                   100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0561521.
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/note= "complementarity determining region 3"
132..140
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                                                                                                                                                                                                                                                                                                                                                                                                                                        83.1%; Score 544; DB 18; 82.6%; Pred. No. 7.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger OJ, Saldanha J,
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                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                               AAB30693
                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
02-APR-2001 (first entry)
                                        AAB30693;
                                                                    AAB30693 standard; Protein; 431 AA.
                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis c treatment. The hAb has reduced immunogenicity, and toxicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     humans, but retains the ability to bind the NR-LU-13 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humanised murine anti-human cancer antigen antibody (Ab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the heavy chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 4; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody therapy and immunodiagnosis
                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-042124/04.
                                                                                                                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain; variable region; murine; mouse; human; cancer antigen;
antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                VSS
                                                                                                                                                                                                                    dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117
                                                                                                                                                                                                                                                                                                                                                                           102;
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aR, Renojm,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AA;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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31..35
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                                                                                                                                                                                                                                                                                                                                                                                      79.9%;
82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                Score 523.5; DB 19; Length 120; Pred. No. 4.9e-41;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Pedersen

NR-LU-13,

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AAW44124 RESULT В QY Дb Qy DЬ ρ

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                                                                                                                                                                                                    Matches 102;
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Best Local
                                                                                                                                                                                                                                                                                                                           and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a fusion of the single chain antibody huNR-LU-10 and streptavidin. The antibody binds the antigen EGP40 or EPCAM. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a first nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A fusion of single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated cancer, e.g. adenocarcinomas – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-2000
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03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptavidin; tumour cell; cancer; adenocarcinoma; hematological malignancy; huNR-LU-10; EGP40; EPCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 10; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avidinii.
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                   148
 265 vss 267
                                                                                                   61
                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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DB; AAC86562.
                                 VSS 123
                                                               DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntks
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                      431
                                                                                                                                                                                                    Conservative
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99US-0168976.
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                                                                                                                                                                                                                    79.9%;
82.9%;
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                                                                                                                                                                                                    8;
                                                                                                                                                                                                                    Score 523.5; DE Pred. No. 2e-40;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin Y,
                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanderson JA,
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                    Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reno JM;
                                                                                                                                                                                                        Gaps
                                                                                                                                      207
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AAR76681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
  Вþ
                    Qy
                                            밁
                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76681 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             medulloblastoma; brain tumour; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
                                                                                                                                                             AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-RVL-M21g(gamma)1. The antibody is reactive with human medullo-blastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                    Reconstituted antibody against human medullo:blastoma cells contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                      Ohtomo T, Sato K,
                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                      Claim 26; Page 94; 120pp; Japanese.
                                                                                                                                                                                                                                           antigenicity
                                                                                                                                                                                                                                                                                       N-PSDB; AAQ94539
                                                                                                                                                                                                                                                                                                 WPI; 1995-200347/26.
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                           (CHUS ) CHUGAI SEIYAKU KK
80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133
                                            20
                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                         qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79
                                                     OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                        103;
                                                                                                Similarity
                                                                                                                                             136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                  93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                        94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= FR 1
51..55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR 1
56..59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= FR 3
119..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR 2
87..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= FR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= FR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR 3
                                                                                                                                                                                                                                                                                                                       Tsuchiya
                                                                                                79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                        4; Mismatches
                                                                                                  Score 523; DB 16;
Pred. No. 6.2e-41;
                                                                                          10;
                                                                                                            Length 136;
                                                                                          6;
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2.

ρy

121 VSS ||| 134 vss

Ъ

136 123

6,

Gaps

2

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AAW04396
                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Sequence
            e.g. myeloblastoma.
                                                                                                     Example 5; Pages 38-39; 45pp; Japanese.
                                                                                                                                           N-PSDB; AAT38653.
                                                                                                                                                                          18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                           18-NOV-1994;
                                                                                                                                                                                                        02-JUL-1996.
                                                                                                                 treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                    JP08169900-A
                                                                                                                                                                                                                                                                                                                       Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity;
                                                                                                                                                             (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                  diagnosis; treatment; cerebral tumour; reshaped
                                                                                                                                                                                                                                                                                                                                                        09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                      AAW04396;
                                                                                                                                                                                                                                                                                                                                                                                AAW04396 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                 1996-358509/36.
136 AA;
                                                                                                                                                                                                                                                                                                                                                       (first entry)
```

118.

.125

/label= mat\_peptide

/label= sig\_peptide

/label= CDR\_1

Location/Qualifiers

/label= CDR\_3 /label= CDR\_2

94JP-0252166. 93JP-0291078. 94JP-0285057

Query Match

79.8%;

Score 523;

DB 17;

Length 136;

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cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                               The present sequence is a fragment of the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric beauty constant region sequences, respectively to produce chimaeric
                                                                                                                                                               human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then
                                                                                                                                                                                                                                                                                                                                                                Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR76682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                     AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the human antibody ONS-M21 FV fragment. The plasmid was used in the construction of an expression vector, contg. cDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be
Sequence
                             used in the diagnosis and treatment of this
                                                                                                                                         Claim 35; Pages 98-99; 120pp; Japanese.
                                                                                                                                                                               antigenicity
                                                                                                                                                                                         Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and
                                                                                                                                                                                                                                                                                                                                                            19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1995.
                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                              Ohtomo T,
                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric medulloblastoma; brain tumour; treatment; diagnosis; Fv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ONS-M21 antibody Fv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR76682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR76682 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 vss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn----qdywgqgttvt 133
                                                                                                                                                                                                                                                              1995-200347/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103;
                                                                                                                                                                                                                                              AAQ94548
                                                                                                                                                                                                                                                                                             Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                            93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                           94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "
140..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "FLAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262..269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= sig_peptide
                                                                                                                                                                                                                                                                                           Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "light variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "heavy variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                         disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                           cells -
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protein;
fragment.

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RRESULT 7
ID AAWW XX
AAW AAWW XX
O9-1
XX Mur
XX N
PFT Reg
FT Pep
FT Pep
FT Pep
FT Reg
FT N
XX N
PFT N
XX N
PFT Reg
FT Reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimaeric human/murine MAb ONS-M21 scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04397 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine; human; myeloblastoma; chimaera; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
The present sequence is a scFv fragment from the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP08169900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 vss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSS 123
                                                                                                                                                                                                                                                           Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT38662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                 Example 6; Pages 40-41; 45pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
                                                                                                                                                                                                                                                                                                                                                                                                  1996-358509/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0252166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94JP-0285057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155..261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "light variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "heavy variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. myeloblastoma.
The sequence encodes the mouse antibody 21.6 heavy chain variable region, HC, directed against leukocyte adhesion molecule VLA-4. Cloned region like the constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse by the amino acid present in the equivalent position of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81325 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1995
                                                                                                                                                                                    Claim 13; Page 70; 105pp; English.
                                                                                                                                                                                                                                                    New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                       WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 vss 139
                                                                                                                                                                                                                                                                                                                       Bendig MM,
                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                     inflammatory disease
                                                                                                                                                                                                                                   leukocyte adhesion to endothelial cells, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                       Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         94US-0186269
                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US01219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                            Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 523; DB 17;
Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                            Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                              for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                   Misc-difference
                                                                              Region
                                                                                                                     Region
                                                                                                                                                             Region
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                       asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                 Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised alpha-4 integrin antibody 21.6 VH HC
                                                                                                                                                                                                                                                                                                                                                            Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                              atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22426 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. The meningitis or encephalitis. The antibodies can also be used for the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLYQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                               Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                  /note= "21/28'CL framework region 1" 27..30
/note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                  /note= "21/28'CL framework region
50..66
                                                                          /note= "21.6 complementarity determining region 67...98
                                          /note= "21/28'CL framework region
                                                                /label= FR3
                                                                                                                                             /label= FR2
                                                                                                                                                              /note= "21.6 complementarity determining region
                                                                                                                                                                                                                              /note= "21/28'CL residues 27-30 are replaced by
                                                                                                    /label= CDR2
                                                                                                                                                                                  /label= CDR1
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                /label= FR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.6%;
82.9%;
                                                                                                                                                                                                             pinding,
                                                                                                                                                                                                                      those of MAb 21.6, involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 515; DB 16;
Pred. No. 2.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                   in antigen
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                                                                                                                                                                                                                                                                         This polypeptide, designated HC, comprises the heavy chain variable CC cregion (VH) of a humanised alpha-4 integrin antibody 21.6. It is CC composed of complementarity determining regions (CDRs) from the VH CC region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody C2.6 and a modified human 21/28/CL framework. It contains an antibody CC additional amino acid substitution (Tyr102Phe) in comparison to CC claimed humanised 21.6 VH version Ha (see AAW22412). Humanised CC 21.6 VH and VL regions are used to produce claimed humanised 21.6 CC antibodies useful in the manufacture of a medicament for treating CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory CC bowel disease, thmour metastasis, nephritis, atopic CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte CC mediated lung injury. The humanised antibodies have a half-life CC in the human circulation essentially equivalent to that of CC nafirally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 102;
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                 naturally occurring human antibodies
117 vss 119
                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma, atherosclerosis, AIDS, dementia, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 7; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1995;
                                                 61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997.
                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9718838-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                       Local Similarity
                                                                                                              qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60
                                                                                                                                                                                                                                                                      119 AA;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0561521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US18807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= FR4
/note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "21/28'CL Tyr-102 is substd. by Phe of human VCAM-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "21.6 complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR3
                                                                                                                                                                                                   78.6%;
82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leger OJ, Saldanha J, Yednock TA;
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                                                                                                                                                                                      5,
                                                                                                                                                                                  Score 515; DB 18; Length 119;
Pred. No. 2.9e-40;
5; Mismatches 12; Indels
                                                                                                                                                                                Indels
                                                                                                                                                                                  4.
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Search completed: May Job time: 247 sec

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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                              491.5
489.5
489.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123
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655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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PCT-US95-01219-9
US-08-561-521-4
PCT-US95-01219-4
US-08-646-265A-132
US-08-646-265A-132
US-08-646-265A-132
US-08-561-521-13
PCT-US95-01219-13
PCT-US95-01219-12
PCT-US95-01219-12
PCT-US95-01219-14
PCT-US95-01219-14
US-08-232-081B-8
US-09-025-769B-36
US-09-025-769B-59
US-09-025-769B-59
US-08-836-561-63
US-08-137-117D-112
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US-08-290-592E-17

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PCT-US96-09448-17
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Sequence 13, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 44, Appl
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Sequence
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Sequence 99, Appl
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sequence 36, App
        Sequence 112,
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ALIGNMENTS

## RESULT 1 US-08-561-521-11 ; Patent No. 5840299 , MOLECULE TYPE: protein US-08-561-521-11 Sequence 11, GENERAL INFORMATION: Query Match Best Local Similarity TELEFAX: 415-543-5043 INFORMATION FOR SEO ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 123 amino acids PILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 1527 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600 APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 APPLICANT: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION UNMBER: US/08/186,269A FILLING DATE: 25-JAN-1994 CITY: San Francisco COUNTRY: FILING DATE: APPLICATION NUMBER: US/08/561,521 TOPOLOGY: STRANDEDNESS: TYPE: 94105 Application US/08561521 amino acid California USA Bendig, Mary M. linear Floppy disk single 100.0%; 15270-14 Score 655; DB 2; Pred. No. 1.7e-58; Length 123;

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PCT-US95-01219-11
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186.
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, VGCURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

Stenart Tower, Suite 2000
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NUMBER OF SEQUENCES: 45
                                                                                          / Match 100.0%; Score 655; DB 5; Length 123; Local Similarity 100.0%; Pred. No. 1.7e-58; nes 123; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 Mismatches

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PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
ETLING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30.22
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                                                                                                   140 VSS 142
                                                                                                                                        121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                         80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139
                                                                                                                                                                          61 DPKEQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLYT 120
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NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                              20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79
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100.0%; Score 655; DB 2
Local Similarity 100.0%; Pred. No. 2e-58;
hes 123; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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One Market Plaza, Steuart Tower, Suite 2000
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Townsend and Townsend Khourie and Crew

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                                                                                                                 Sequence 9, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Jones, S. Tarran
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%; Score 655; DB 5; Length 142; Local Similarity 100.0%; Pred. No. 2e-58; ses 123; Conservative 0; Mismatches 0; Indels
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                Bendig, Mary M.
Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 25-JAN-1994
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                                                                                                                        APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
MUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Khourie and Crew
ATREET: One Market Plaza, Steuart Tower, Suite 2000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: On
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                       COUNTRY:
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US-08-561-521-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4,
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ADDITION TON DATA:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Humanized Antibodies Agrantice of INVENTION: Adhesion Molecule VLA-4
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                               APPLICATION NUMBER: US/08/561,521
                                                      FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                        MEDIUM TYPE:
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Leger, Olivier J.
Saldanha, Jose
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US/08/186,269A
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PCT-US95-01219-4
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                TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
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APPLICANT: Jones, S. Tarran
              TELEPHONE: 415-543-5043
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L,
REGISTRATION NUMBER: 30,223
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                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                               94105
                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                          California
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                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig, Mary M.
Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                    25-JAN-1995
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82.6%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                             Release #1.0, Version #1.25
                                                                                                                                                  US 08/186,269
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LENGTH:

140 amino acids

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US-08-646-265A-132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                           INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ON-THOMO, TOSNIIIAN
APPLICANT: SATO, KOh
APPLICANT: TSUCHIYA, MASAYUKİ
APPLICANT: TSUCHIYA, MASAYUKİ
APPLICANT: TSUCHIYA, MASAYUKİ
APPLICANT: TNVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
                                                                                                                                             NAME: WECNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE_DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,672-5300
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
                 MOLECULE TYPE:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 300.
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                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO PILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                   904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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3000 K Street, N.W., Suite 500
                                                                                                                                 (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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               protein
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                              Query Match
Best Local Similarity
Matches 103; Conserv
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Patent No. 6
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                                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: V
FILING DATE: 19-0CT-
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
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                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C
REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08 FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                           TYPE:
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                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                             (202)672-5399
                                  Conservative
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                                                                                                                                                         linear
                                                                                                                                       protein
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                                                79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
132
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83.7%;
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                                Score 523; DB 4; Length 136;
Pred. No. 2.9e-45;
4; Mismatches 10; Indels
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Pred. No. 2.4e-45;
4; Mismatches 10
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GENERAL INFORMATION:
                                                                                                                                               Matches
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,265A FILLING DATE: 09-58F-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RESHAPED HUMAN ANTIBOUTITLE OF INVENTION: MEDULLOBLASTOMA CELLS NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/JP94/01763 FILING DATE: 19-OCT-1994 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 136
                                                                     23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82
                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                      TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                             103;
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                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                           Conservative
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83.7%;
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                                                                                                                                                                                                                                                                                                                                          109:
                                                                                                                                           4; Mismatches 10; Indels
                                                                                                                                                       Score 523; DB 4; Length 269; Pred. No. 6.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                  53466/184
                                                                                                                                        Gaps
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RESULT 13
PCT-US95-01219-13
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; MOLECULE TYPE: protein US-08-561-521-13
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US-08-561-521-13
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
FENGTH: 119 amino acids
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/186,269A FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized Antibodies Ag
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
117 VSS 119
                                      121 VSS 123
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                                                                               61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116
                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Leger, Olivier J.
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82.9%;
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US-08-561-521-12
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-13
                                                                                                                    Sequence 12, Patent No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 102; Conservative
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                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
                                                                 APPLICANT:
APPLICANT:
                                 APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/11
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humanized Antibodies ay.
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                        117 VSS 119
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                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                   Application US/08561521
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                              Bendig, Mary M.
Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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Humanized Antibodies Against Leukocyte Adhesion Molecule VLA-4
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82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
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RESULT 15
PCT-US95-01219-12
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                                                                                                                                                                                                                                                                               Sequence 12, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                               APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                            TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
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APPLICATION NUMBER: US/0
FILING DATE: 25-JAN-1994
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                121 VSS 123
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                                                                      STREET: One Market F
CITY: San Francisco
                                   COUNTRY:
                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYYGS----GSNYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
                     94105
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                                                      California
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                                       USA
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82.9%;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOXET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-9043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-12
Search completed: May 7, 2002, 12:23:04 Job time: 175 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                 117 VSS 119
                                                                                                                                      121 VSS 123
                                                                                                                                                                      CLASSIFICATION:
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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                   No.
 15
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                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                   488.5
477
                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                       447
446.5
                                                                                                                                                                                                                                  459.5
456.5
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439.5
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455
450
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655
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Copyright (c) 1993 - 2000 Compugen Ltd.
 PIR_68:*
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pir3:*
pir4:*
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                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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248.659 Million cell updates/sec
                                                                                                                                    Ig heavy chain V-D
anti-Sm antibody V
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g heavy chain V-D
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g heavy chain V r
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g gamma chain V r
g gamma chain V r
g gamma-1 chain r
g heavy chain V r
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30 30 30 30 30 30 30 30 40 40 40 40 40
433 433 439.5 429.5 427.5 427.5 427.427 427 427.427 427.426 424.5 424.5 424.5 420.5
66.1 65.8 65.6 65.3 65.3 65.0 64.9 64.3 64.3
127 135 108 108 125 125 127 127 127 127 127 143 144 144 144
$\alpha$
PH0953 PH0953 PH0957 PH1012 PH10157 PH10957 PH10957 PH10957 PH1561 S36010 A33548 S36010 A33548 S36060 PH1561 S23623 S38950 S40295 PH1426 S40295 PH1426 S20783
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heavy heavy
chain V r chain V I chain V I
V v r r v r r v r r v r r v r r v r r v r r v r r v r r v r r v r r v r r r v r r r r v r

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Ig gamma chain (WM65) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S29594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S29593
A; Accession: S29594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, February 1991
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A; Residues: 1-178 <SEY>
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                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                              B
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983 A;Ote: this sequence was determined from the differentiated gene R;Rocca-Serra, J.: Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982
                                                                                                                     A; Reference number: S03471; MUID:84057768
A; Accession: S03471
                                                                                                                                                                                      A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                                                                                                                                                                                                                           S03471
                                                                                 A; Molecule type: mRNA
A; Residues: 7-120 < ROC1>
                                                                                                                                                                      hypervariable regions.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYMGQGTSVT 128
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R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
                                                                                                                                              C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
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                                                                                                                                                                                                                                                                           Ig heavy chain V-1 region (WIL2) - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;15-98/Domain: immunoglobulin homology <IMM>
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A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448
A;Recession: S36256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-118 <GRI>
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C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown
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76.2%;
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75.6%; Pred. No. 6.3e-36; ...
''' Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches 13; Indels 11; Gaps
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Pred. No. 1.3e-35;
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R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                        Ig heavy chain V region (EB) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S17586
                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-142 <LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells A;Reference number: A32483; MUID:89273586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - human (fragment)
c;Species: Homo sapiens (man)
c;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
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C;Keywords: heterotetramer; immunoglobulin
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A;Accession: D33548
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                                                                                                                                                                                                                                                                                131 TLVTVSS 137
                                                                                                                                                                                                                                                                                                                         117 TLVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                           61 DEKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----GYYGNYGVYAMDYWGOG 116
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73.2%;
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74.8%;
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Pred. No. 4.1e-35;
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A; Reference number: S17586; MUID:92015240 A; Accession: S17586

A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-117 <MYL>

Query Match Best Local

Similarity

71.0%; Score 465; DB 2; Length 117; 72.6%; Pred. No. 7.3e-35;

Matches

90;

Conservative

15;

Mismatches

11; Indels

8

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1;

61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119 

1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60 A;Cross-references: EMBL:X60683; NID:951820; PIDN:CAAA3095.1; PID:951821 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

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R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531
A;Accession: S06823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: pH0952; MUID:92202880
A;Accession: pH0954
A;Status: nucleic acid sequence not shown
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A; Residues: 1-132 < MAR>
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F;36-50/Region: framework 2
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F;68-98/Region: framework 3
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C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Moncharmont, B. submitted to the EMBL Data Library, September 1991 A;Description: Cloning and sequencing of the cDNA coding for the variable regions of A;Description:
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A; Accession: S24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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S49220
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                                                                                   114 VSS 116
                                                                                                                          121 VSS 123
                                                                                                                                                                61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY-----FDYWGQGTTLT 113
                                                                                                                                                                                    62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                          88;
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                                                                                                                                                                                                                                                                                                                                     69.5%; Score 455; DB 2; Length 116; nilarity 71.5%; Pred. No. 5.7e-34; Conservative 13; Mismatches 14; Indels
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72.0%;

    Mismatches

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Pred. No. 4.8e-34;
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Ig heavy chain V region (clone IIc) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000 C;Accession: S06823

A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-122 <MIL>

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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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                              Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
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  R; Martin,
J. Exp. M
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Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
Exp. Med. 175, 983-991, 1992
                                                                                                                                                                                            119 TVSS 122
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                                                                                                                                                                                                                                                                                                                       F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
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J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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F;1-120/Domain: V region #status predicted <VRG>
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A;Residues: 1-221 <KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a A;Reference number: S49220
A;Accession: S49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
121 KGTTVTVSS 129
                                        115 QGTLVTVSS 123
                                                       61 AOKFOGWYTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120
                                                                              61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VSS 123
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASYKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVKLLESGAELVKSGASVKLSCTASGENIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 70.7%; Score 455; DB 2; Length 221; Conservative 12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region #status
                                                                                                                                                                                                                 68.7%; Score 450; DB 2; Length 129; 70.5%; Pred. No. 1.8e-33; ative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted <CRG>
                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-135 < MA)
                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                   anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                       A; Accession: S49530
                                                                                                                                                                                                                                                                                                                                       A; Reference number: S48797
                                                                                                                                                                                                                                                                                                                                                                    R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                          A; Description: Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                    Matches 91; Conservative
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-43 < ROC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this sequence was determined from the differentiated gene R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A;Accession: S07453; MUID:83058021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: mRNA
A:Residues: 10-115 <ROC1>
A:Cross-references: EMBL:X03219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment) C:Species: Mus musculus (house mouse) A;Variety: strain BALB/c C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C:Accession: S03482; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03482
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  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 V 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFOGKATITTDTSSNTAYLQESSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLOGSGAELVKPGÁSVKLSCTASGFNIKDTYMHWVKORPEOGLEWIGRIDPAKGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
HIHHHHHHHHHH:
                                                                                                                                                                                                                                                  1-135 <MAH>
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                                                         68.3%; Score 447.5; DB 2; 72.8%; Pred. No. 3.1e-33; ative 7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.5%; Score 449; DB 2; 70.2%; Pred. No. 1.9e-33;
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                                                    Indels 11;
                                                                                                   Length 135;
                                               Gaps
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A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
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S03484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S07453; MUID:83058021
A; Accession: S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Rocca-Serra, J.; Mazie, J.C.; Moinler, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: this sequence was determined from the differentiated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 10-120 < ROC1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                            R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                      Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
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A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC -- AREGYYGNYGVYAMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 68.2%; Score 447; DB 2; Length 120; Local Similarity 71.5%; Pred. No. 3e-33; ss 88; Conservative 11; Mismatches 20; Indels
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Job time: 199 sec

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F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1 F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1
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Search completed: May 7, 2002, 12:23:48
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Best Local S
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                                                                                  121 YGMDVWGQGTTVTVSS 136
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                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-------EGYYGNYGV 107
                                                                                                                                                                61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120
                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     framework 2
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                  68.2%;
69.1%;
                                                                                                                                                                                                                                                                                                                                 1; Mismatches 28;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                        No.
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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396
396
375,5
375,5
371,373
371,373
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364,5
369,5
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349,5
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408.5
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Gapop 10.0 , Gapext 0.5
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655
100059 segs, 36664827 residues
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                  DB
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HV13_MOUSE
HV51_MOUSE
HV11_MOUSE
HV11_MOUSE
HV11_MOUSE
HV48_MOUSE
HV48_MOUSE
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HV51_MOUSE
HV51_MOUSE
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HV03_MOUSE
HV07_MOUSE
        HV1H_HUMAN
HV0H_MOUSE
HV00_MOUSE
HV06_MOUSE
HV16_MOUSE
HV16_MOUSE
HV11_MOUSE
HV14_MOUSE
HV24_MOUSE
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HV37_MOUSE
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HV02_MOUSE
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p06329 mus musculu
p01745 mus musculu
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p06326 homo sapien
p80421 homo sapien
p80421 homo sapien
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p01761 homo sapien
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5 mus musculu
                                                                                                                                                                                                                                                                             homo sapien
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Qy Qy

Query Match 65.3%; Score 427.5; DB 1; Best Local Similarity 64.1%; Pred. No. 6.6e-36; Matches 82; Conservative 16; Mismatches 25;

DB 1; Length 147; se-36; s 25; Indels 5

5; Gaps

1:

DR PIR; A0200 DR InterPro; DR InterPro; DR Ffam; PF00( DR SMART; SM KW Immunoglol FT SIGNAL FT CHAIN FT CONFLICT CONFLICT FT C	ÇĞ	34 318 35 318 36 37 37 37 37 37 37 37 37 37 37 37 37 37
26; E1HU 1FR0035 IPR0035 O047; ig 100406; ig 100406; ig 20 20 20 21 53 67 125 147 AF	STANI (Rel. 4) (Rel.	19 48.7 .5 48.6 118 48.4 1.5 48.1 1.5 48.1 1.5 48.1 1.4 47.9 1.13 47.8 1.12 47.6 1.12 47.6
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IG HEAVY CHAIN V-I REGION PYRROLIDONE CARBOXYLIC ACT -> V (IN REF. 2). IH -> HI (IN REF. 2). VG -> GV (IN REF. 2). MISSING (IN REF. 2). M1SSING (IN REF. 2).	date) (FRAGMENTS). ; Vertebrata; ni; Hominidae; ni; Hominidae; ni a myeloma 6665(1982). hr-Lindstrom Hoepts and deve	N
REGION ND. LIC ACID. )).	ta; Euteleostomi; dae: Homo.  ire R.B., Viney J., for the human oma cell line."; om H.; developments, pp.1-36, ed FROM A MYELOMA	PO1812 mus musculu PO1762 homo sapien PO1771 homo sapien PO1787 mus musculu PO1787 mus musculu PO1790 mus musculu PO1794 mus musculu PO1794 mus musculu PO1805 rattus norv PO1809 mus musculu PO1791 mus musculu PO1791 mus musculu PO1791 mus musculu PO1791 mus musculu PO1769 homo sapien

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"The genetic basis of antibody production: the dominant anti-arsonate ridiotype response of the strain A mouse.";

RI "The genetic basis of antibody production: the dominant anti-arsonate ridiotype response of the strain A mouse.";

RI Eur. J. Immunol. 12:1023-1033(1982).

CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J CC SEGMENT, JH2.

CC SEGMENT, JH2.

CC SEGMENT, JH2.

CR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003059; Ig_WHC.

DR InterPro: IPR003059; Ig_V.

RV Immunoglobulin V region; Antiarsonate antibody; Hybridoma.

REPOILED TO THE SAME J CONCLUDE TO THE SAME J CROUTER TO THE SAME J CROUTER TO THE SAME J CROUTER TO THE SAME J CROUTER TO THE SAME J CROUTER TO THE SAME J CROUTER TO THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CROTHS THE SAME J CR
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HV03_MOUSE
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Best Local :
                                                                                                                                            HVO7_MOUSE STANDARD; PKT; LJ7 GA., P01751; P01752; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1990 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
STRAIN=C57BL/6;
                        SEQUENCE FROM N.A.
                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
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MEDLINE=83131846; PubMed=6186498;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION 36-65.
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                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
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63.1%;
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No. 3.7e-34;
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HV1B_HUMAN
ID HV1B_HUMAN
AC P01743;
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                SEQUENCE FROM N.A.
MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Za
                                                                   Eukaryota; Metazoa; Cnordata; cranraca, cracca, Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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SMART; SM00406; IGV; 1.
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-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltimore D.;
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                                                                                                                                                                                                                                                                                                             20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
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Pred. No. 4.9e-34;
                                                                                         Craniata; Vertebrata; Euteleostomi;
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JH2 SEGMENT
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                Zakut R.,
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                Givol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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InterPro; IPR003006; Ig_MHC
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smarr; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V REGION 9367 PRECURSOR.
Mus musculus (Mouse).
Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV02_MOUSE
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                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Local Similarity 79.6%;
                                                                                                                                                                      EMBL; J00493; AAA38128.1; -. PIR; A02028; HVMSG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
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         SMART; SM00406;
                                                                                       InterPro; IPR003596; Ig_v.
                                                                                                                                 InterPro; IPR003006;
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                                                  PF00047; ig; 1.
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         IGv; 1.
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01-NOV 1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Dispersed localization of D segments in the human immunoglobulin heavy-chain locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88296408; PubMed=2841108;
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smarr; sm00406; IGv; 1.
Immunoglobulin V region; Signal.
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Interpro; IPR003596; Ig_v.
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20 QVQLVQSGAEVKKPGASVKVSCKASGYTETGYYMHWVRQAPGQGLEWMGRINPNSGGTNY
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                               1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTVIHWVRQAPGORLEWMGRIDPANGYTKY 60
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75; Conserv
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78.6%;
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                                                                                           Score 396; DB 1;
Pred. No. 7.1e-33;
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    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION J558
                                                                           HV13_MOUSE
                                                                  P01757;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; nothemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01742;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-I REGION EU
                                                                                                                                                                                61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFIDE BOND
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 musculus
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MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MIELOMA PROTEIN HAS ALSO BEEN DETERMINED.
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117 117
117 AA; 12472 MW;
(Mouse).
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                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                               Score 390; DB 1; Length 117; Pred. No. 2.8e-32;
                                                                       PRT;
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HV51_MOUSE
ID HV51_MOUSE
AC P06330;
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             SEQUENCE
                                   DISULFID
                                                                                                                                                            MEDLINE-84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
                          NON_TER
                                                   DOMAIN
                                                                      Immunoglobulin V region.
                                                                                                  Pfam; PF00047; ig;
SMART; SM00406; IG
                                                              DOMAIN
                                                                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00047; ig; 1.
SMART; SW00406; IGv; 1.
Immunoglobulin v region.
DISULFID 22 96
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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 205.12.
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01-JAN-1988 (Rel. 06, Last sequence)
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments."; Nature 283:35-40(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120 : | | | | | | | | 120
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117 AA;
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118
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12934 MW; 94F7BEE4C762A018 CRC64;
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RESULT 10
HV12_MOUSE
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AC P01756
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RESULT 11
HV11_MOUSE
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21-JUI-1986 (Rel. 01, Last sequence update)
15-JUI-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION MOPC 104E.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE:
MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pF00047; 19; 1.
smART; sM00406; IGv; 1.
Immunoglobulin V region; Glycoprotein.
prsuterD 22 96 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                        115 VSS 117
                                                                                                                                                                               121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 56.9%; Score 373; DB 1; Length 117; Local_Similarity 59.3%; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN HAS ALSO BEEN DETERMINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 57.3%; Score 375.5; DB 1; Similarity 58.5%; Pred. No. 8e-31; 72; Conservative 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
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55
117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                   RESULT
                                    HV48_MOUSE
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                         Query Match
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P01755; P01755; P17986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

15-JUL-1999 (Rel. 38, Last annotation update)

16 HEAVY CHAIN V REGION S43 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. Between the Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heavy chain variable region contribution to the NPb family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 19; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02038; G2MS43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00539; AAA38172.1; -.
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SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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P03980;
23-OCT-1986 (Rel. 02, Created)
                         HV48_MOUSE
                                                                                               135 VSS 137
                                                                                                                         121 VSS 123
                                                                                                                                                                                                          20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS:
                                                                                                                                                                 80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134
                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                         137 AA;
                                                                                                                                                                                                                                                                   Conservative
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                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                 49
54
68
85
117
122
137
                                                                                                                                                                                                                                                                                                                                         15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                   56.7%; Score 371.5; DB 1; Length 137; 60.2%; Pred. No. 2.4e-30;
                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING 1.
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RESULT 13
HV50_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
               MEDLINE-84182519; PubMed-6201362; Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in lymphocytes is encoded by a large set of antibody structural genes EMBO J. 3:517-523(1984).

PIR: A02037; MHMS15.
                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 15.3.
            InterPro;
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               P06329;
                                                                                                                                                                                                                                                                                                                                                                                                                                              HV50_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Illegitimate recombination generates a class switch from C mu to delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF-----VYWGQGTLV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=84248078; PubMed=6429663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79
IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%; Score 369; DB 1; Length 138; 58.1%; Pred. No. 4.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION TEPC 1017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA.
                                                        structural genes.";
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin v region.
DOMAIN 99 105
DOMAIN 99 105
DOMAIN 106 120
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 121 121
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Nucleic Acids Res. 8:4839-4840(1980).

-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zakut R., Cohen J., Givol D., "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=81053741; PubMed=6253904;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MPC 11.
61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                   1 EAGLQOSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01745;
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                                                                                                                                                                                               55.0%;
                                                                                                                                                                                                                                                                                   13135 MW; 227AEF3EC56ED0BF CRC64;
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56.1%;
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                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                     Score 360; DB 1;
Pred. No. 2.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
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Pred. No. 1e-29;
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Search completed: May 7, 2002, 12:32:34
Job time: 565 sec
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Best Local Similarity
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMARP; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. V REGION BCL1 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way madified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared
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                                                                           134 VSS 136
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                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                       136
136 AA;
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                       136 IG HEAVY CHAIN V REGION D.
136
15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                           55.0%; Score 360; DB 1; Length 136; 56.9%; Pred. No. 3.3e-29;
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OM protein - protein search, using sw model
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries
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Q99298 homo sapien
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Q9u195 homo sapien
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Q9j185 mus musculu
Q9u194 homo sapien
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01-MAY-2000 (TIEMBLIE1. 13, Last sequence update)
01-JUN-2001 (TIEMBLIE1. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE
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                                                                                                                                                                                                                                   EMBL; AF035022; AAD56258.1; -.
Interpro; IPR003006; Ig_MC.
Interpro; IPR003596; Ig_v.
pfam; PF00047; id; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
Clin. Immunol. ImmunoGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               Young D.C
                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                           y Match 69.8%; Score 457.5; DB 4; Length 124; Local Similarity 69.5%; Pred. No. 5.1e-40; hes 91; Conservative 9; Mismatches 16; Indels 15;
61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM-------DY 112
                                                  1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                  DOMAIN.
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                                                                                                                                                                                          124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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Q99L31
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                            SEQUENCE
                                                                                                                                                                                                                                                         Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                           SMART; SM00406; IGV; 1.
                                                                                                                                         EMBL; AF206021; AAF69319.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                        Pfam; PF00047; 1g; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNCLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C;
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submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
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Q99L31;
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                                                                                                                                                                                                                                  SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                    109 AA;
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11944 MW; DFE615FE6CED4EDE CRC64;
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67.5%;
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Pred. No. 1.7e-37;
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                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TIEMBLIE1. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                              Q9GYZ2;
                                                                                           Q9GYZ2
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SEQUENCE
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InterPro; IPR003596; Ig_v.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                       61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                              61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR-----GAVVFDYWGQGTALTVSS 109
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                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                     66.0%; Score 432; DB 4; Length 119; 70.7%; Pred. No. 2.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                              119 AA.
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                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song X.T., Feng Z.Q., Guan X.H.;
Song X.T., Feng Z.Q., Guan X.H.;
Song X.T., Feng Z.Q., Guan X.H.;
Song X.T., Feng Z.Q., Guan X.H.;
Samplification, cloning and sequence analysis of the heavy chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.;
Schistosoma japonicum.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
schistosoma japonicum (Blood fluke).
schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 19; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003600;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                         Q9UL95;
Q9UL95;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMINOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                              Young D.C.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VSS 123
                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKEKDRYTMTTDKSESTAYMDLRSLKSADSAVYYCAR--YYDDH--YCLDYWGOGTTVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                        EMBL; AF035019; AAD56255.1; -
                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60
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           InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
InterPro; IPRO03596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
NON TER
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                                                                                                     SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSS 119
                                                                                          DOMAIN
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                                                                                                                                                                              Liu B., Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.3%; Score 428; DB 5; Length 119; 66.7%; Pred. No. 5.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig_MHC.
                                                                                                                                                                                    der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Indels
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RP STRAIN=C57BL/6J; TISSUE-PANCREAS;

RC STRAIN=C57BL/6J; TISSUE-PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RX Kawai J., Shinagawa A., Shibata K., Kondo S., Yamanaka I.,

RA Arakawa T., Hara A., Fikunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa T., Hara A., Fikunishi Y., Bono H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi X., Kiyosawa H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Colawah H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,

RA Sakai K., Sitaubli F., Suzuki R., Tomita M., Wagarer L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Bake J., Boffelli D., Bojunga N., Carnincic P., de Bonaldo M.F.,

RA Baki H., Sato K., Bojunga N., Fume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kohtsuki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9D814;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9D8L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Mommalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120
                 Interpro: IPR003596; 19_v.

Pfam; PF00047; 19; 4.

Pfam; PF000409; IG; 2.

SMART; SM00409; IGc; 3.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OVOLVQSGAEVKKEGASVKVSCKASGFNIKDTYIHWVROADGORLEWMGRIDDANGYTKY 60
                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                            EMBL; AK007918; BAB25349.1; MGD; MGI:1924014; 1810060005
                                                                                                                                             InterPro: IPR003597; I9_c1.
InterPro: IPR003600; I9_like.
InterPro: IPR003005; I9_MHC.
                                                                                                                                                                                                              InterPro; IPR003599;
    PROSITE;
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        PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                     1810060009Rik.
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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SMART; SM00406; IGV; 1.
                                                                               Q99L25
                                                                                                                                                                                                                                                                                                                     NON_TER
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Q9UL89; PRELIMINARY;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Homo sapiens (Human).

""""" Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                     61 OGRVTÍTÁDKSTSTAYMELSSLRSEDTAVYYCÁS----SNWGDYWYFDLWGRGTLVTVSS 116
                                                                                                                                  65 QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                     1 VÓSGAEVKKÞGSSVKVSCKASGGTESSYAISWVRQAÞGQGLEWNGRIIPILGIANYAQKF 60
                                                                                                                                                                                 5 VOSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGORLEWMGRIDPANGYTKYDPKF 64
                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 NEKFKGKATLTÁDKSSSTAYMQLSSLTSEDSAVYFGÁRSGY--DYDWFA--YWGQGTLYT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVROAPGORLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                     Similarity
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116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
                                                                       PRELIMINARY;
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                                                                                                                                                                                                                         62.8%; Score 411.5; DB 4; Length 72.5%; Pred. No. 2.8e-35; Indels
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                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches 19; Indels
                                                                  473 AA.
                                                                                                                                                                                                                                               DB_4; Length 116;
                                                                                                                                                                                                                      5; Gaps
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Qγ
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                                                                                                                                                                                                                                                      InterPro; IPRO3006; Ig_MHC.
InterPro; IPRO3596; Ig_V.
InterPro; IPRO3596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
NON TER
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OC
OC
OX
OX
RA
RA
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DR
115 VSS 117
                           121 VSS 123
                                                                                                                                                                                                                              NON_TER 117
NON_TER 117
SEQUENCE 117 AA;
                                                                                                                                                                                                                                                                                                                                 Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPOXE9;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HENTY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                               61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----YAMDYWGOGTSVT 114
                                              EMBL; AJ225174; CAB65237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QXE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 ITVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003888; AAH03888.1; ... BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGSIYYG-YGLYYFDYWGOGTT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYAMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRPEQGLEWIGYIYPRDGSTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                13000 MW; CDDE2AF84D499734 CRC64;
                                                                                                                                                         62.1%; Score 407; DB 11; Length 117; 62.6%; Pred. No. 8.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.4%; Score 408.5; DB 1 63.2%; Pred. No. 3.2e-34;
                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 25; Indels
                                                                                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 473;
                                                                                                                                              6,
                                                                                                                                          Gaps
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Q9BRVO
ID Q9BRVO
AC Q9BRVO
DT 01-UUN
DT 01-UUN
DT 01-UUN
DT 01-UN
DT 01-UN
CENKARY
OC ENKARY
OC MAMMAN
OC MAMMAN
CON NCBLT
RN [1]
RN [1]
RN [1]
RN [1]
RN SEQUEN
RC TISSUEN
RC SEQUEN
RA Straus
RA Straus
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Best Local S
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SIGNAL
                                                                                                                                                 Q9BRVO;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:14588).
Homo Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
Strausberg R.;
Strausberg R.;
Strausberg Apr-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 92:496-506(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with
IGG4 monoclonal antibody derived from a hemophilia A patient wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGG VH
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                          Q9BRV0
                                                                                         SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .nhibitor."
                                                                           TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                        DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                              AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-----DPDAFDIWGQGTMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
                                                                                                                                                                                                                                                                                                                                     VSS 136
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                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 399;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                      Catarrhini;
                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                            500 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
.5e-34;
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                                                                                                                                        Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 150;
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RESULT
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Best Local Similarity
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Best Local
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Q9QXF0;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN 2001 (TrEMBLrel. 17, Last annotation update)
01-JUN 2001 (TrEMBLrel. 17, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPRO03006; Ig_MHC.
InterPro: IPRO03596; Ig_v.
Pfam; PFO0047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A.,
Matis L.M., Evans M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z1C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Z1C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                          Q9QXF0
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U78801; AAD00293.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 GTLVTVSS 123
                                                                                                                113 TLTVSS
                                                                                                                                          118 LVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF
                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                   TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYF---
                                                                                                                                                                                               DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
                                                                                                                                                                                                                           QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                      118 AA; 13036 MW;
                                                                                                                118
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                                                                                                                                                                                                                                                                                 Conservative
 (TrEMBLrel. (TrEMBLrel.
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    118
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Pred. No. 3.7e-33;
  Created)
Last sequence update)
                                                                                                                                                                                                                                                                                              Score 386.5; DB 1 Pred. No. 1.1e-32;
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                                           PRT;
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                                                                                                                                                                                                                                                                                                             DB 11;
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Best Local
SEQUENCE
                                          Signal SIGNAL NON_TER
                                                                                                                                                                                                                                                                                                            patient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.", Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VH1 PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                            InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M., Bohlen H., Diehl V., Wolf J., "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                               EMBL; AJ005570; CAA06599.1; -.
                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; iGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ225171; CAB65236.1; -. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrembLrel. 17, Last annotation update) IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
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Pred. No. 1.2e-32;
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136 VTVSS 140
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                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYY--GNYGVYAMDYWGQGTL 118
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                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                           QVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYYIHWVRQPRGQGLEWMGGIGPGVGSTMC 79
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                                                                                                                                                                                   58.6%; Score 384; DB 4; 63.2%; Pred. No. 2.8e-32;
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OM protein - protein search, using sw model
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Perfect score:
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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                            Variable region of Mouse anti-VLA-4 a Human MCP-3 and mu Human IP-10 and mu Artificial synthet
                                                                                                                                          Mouse VLA-4 antibo
Human VLA-4 reshap
Alpha-4 integrin m
ME1-14 light chain
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64.2	6	σ	6	6	6	Ó	0	65.2	65.5	65.7	65.7	65.8	66.0	66.4	66.4	66.5	67.0	67.1	67.1	67.3	68.0	68.3	70.5	73.5	73.5	73.7	74.0	74.0	74.6	74.7		74.7	71 7	
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	Ganglioside GD3 sp	MAD SCH94.03 light	regi	Mouse C4G1 Ig ligh	ant	lonal	IGFAM	acid sequ		ar	¥	3	Anti-human CD23 5E	Ganglioside GD3 sp	Amino acid sequenc	Light (kappa) chai	Ganglioside GD3 sp	Human/murine IL-1	Humanised antibody	Humanized 1308F VL	Ganglioside GD3 sp	TF8-5G9 CDR-grafte	Ganglioside GD3 sp	CD4-specific CDR-9	FWP51 fusion prote	Murine OKT4A light	P ninjens recombi		Anti-qp54 MAD T16	anti-ons4 Mab T16	reposit - FTA fusion	Humanised aipid *	anti-V	

## ALIGNMENTS

AAR81326 RESULT

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AAR81326;

AAR81326 standard; Protein; 126 AA.

PN X TOTAL T Mouse VLA-4 antibody 21.6 light chain variable region. Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; 23-MAR-1996 (first entry) antibody engineering. Key Mus musculus. Region Region Peptide Region Region WO9519790-A1. Region Region Region /note= 55..69 /note= "signal peptide"
21..43 /note= 77..10 /note= 70..76 /note= "framework region 1" Location/Qualifiers /note= 117..1: /note= "framework region 3"
109..116 /note= .108 ..126 "complementarity determining region 1" "complementarity determining "framework region 2" "framework region 4" "complementarity determining region 3" region 2

AAR78970

Light chain variab

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the mouse antibody 21.6 light chain variable C region directed against leukocyte adhesion molecule VLA-4. Cloned 1 liked to human constant regions in the construction of a humanized c modified using PCR primers (See AAQ99895-98) and them subcloned into CC constant regions. In the humanizing human kappa or gamma-1 c c constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the humanized light chain, amino acids L45, CC by the amino acid present in the equivalent position of the mouse CC constant regions. The humanized light chain, amino acids L45, L58 and L69 in the human kappa LC vR framework are replaced CC lafg L chain. Plasmids encoding the chimeric antibodies are complaced consisted into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and cc to treat inflammatory diseases such as multiple sclerosis. They menigitis or encephalitis. The antibodies can be used for meningitis or encephalitis. The antibodies can be used for detecting VLA-4, for affinity purification or for generating cc anti-1diotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Homo sapiens
                           antibody engineering.
                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                             Human VLA-4 reshaped antibody 21.6 light chain variable region.
                                                                                                                                                                    AAR81332 standard; Protein; 126 AA
                                                                                                          23-MAR-1996 (first entry)
                                                                                                                                                                                                                                                             121 tkleik 126
                                                                                                                                                                                                                                                                                            121 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        61 gkrprilihytsaiqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120
                                                                                                                                                                                                                                                                                                                          61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTEGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ99889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0186269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 680; DB 16; 100.0%; Pred. No. 1.2e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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61 gkrprilihytsalqpgipsrfsgsgsgrdysfnisnlepediatyyclqydniwtfggg 61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

mrpsiqflglllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp 60

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Matches 126;
                                                                              Query Match
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                                                                                                                        human kappa or gamma-l constant regions. In the human kappa IC variation, amino acids L45, L49, L58 and L69 in the human kappa LC varianework are replaced by the amino acid present in the equivalent chimeric antibodies are transfected into COS cells. The humanized enotherical cell and to treat inflammatory diseases such as stroke, cerebral traumas, meningitis or encephalitis. The purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule VIA-4. Cloned cDNA sequences of mouse 21.6 VI (AAQ9888) and VH (AAQ99892) regions are linked to human constant regions in the construction mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing them.
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 10; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ99893
1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVT1TCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1994;
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                                                                                                                  126 AA;
                                                Conservative
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/note= "complementarity determining region 3"
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77..10
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70..76
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                                                    100.0%; Score 680; DB 16; 100.0%; Pred. No. 1.2e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leger OJ, Saldanha J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "framework region 2"
                                              0;
                                            Mismatches
                                         Indels
                                                                Length 126;
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This polypeptide comprises the light chain variable region (VL) mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
metastasis; inflammatory bowel disease; rheumatoid arthritis;
transplant rejection; graft versus host disease; nephritis;
atopic dermatitis; psoriasis; myocardial ischaemia;
                                                          Uses of humanised alpha-4 integrin antibody -asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                  Bendig
                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute Leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-4 integrin mouse MAb 21.6 VL region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1997
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                                     Claim 18; Page 68; 107pp; English.
                                                                                                 WPI;
                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                         21-NOV-1995;
                                                                                                                                                                           21-NOV-1996;
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                                                                                      1997-297879/27
DB; AAT74759.
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                                                                                                                                                        95US-0561521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediated lung injury; therapy.
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55..69
                                                                                                                                                                                                                                                                                                                                                                                                      /note=
44..54
                                                                                                                                                                                                                                                       /note= "complementarity determining region
117..126
                                                                                                                                                                                                                                                                                                                 /note= "complementarity determining
77 .108
                                                                                                                                                                                                                                    /note= "framework region
                                                                                                                                                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                                                                                                                                      /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                        /label= FR1
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                                                                                                                   ST,
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                                                                                                                                                                                                                                                                                                                                                    "framework region
                                                                                                                                                                                                                                                                                                                                                                                                              "framework region
                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region
                                                                                                                   Leger OJ,
                                                                                                                                                                                                                                                                                                       FR3
                                                                                                                                                                                                                                               FR4
                                                                                                                                                                                                                                                                           CDR3
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                                                                                                                   Saldanha
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6 antibody that is used in the munifacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour
                                                                Method of treating solid or cystic tumours with antibodies administering monoclonal antibody Mel-14, having Fc deleted using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equivalent to that of naturally occurring human antibodies.
                                                                                                                     WPI; 1994-316669/39
N-PSDB; AAQ73537.
                                                                                                                                                           Bigner DD,
                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR60627 standard; Protein;
            The sequence is that of the ME1-14 light chain.
                                     Disclosure; Fig 2; 31pp; English
                                                                                                                                                                                     (BIGN/) BIGNER D D.
(CARR/) CARREL S.
(ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                          19-MAR-1993;
                                                                                                                                                                                                                                                                   14-MAR-1994;
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les 126; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA;
                                                                                                                                                            Carrel
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                                                                                                                                                                                                                                            93US-0033864
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                                                                                                                                                             Zalutsky MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 680; DB 18;
Pred. No. 1.2e-47;
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monoclonal antibody which can be administered to treat solid

protein

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AAW22419
ID AAW2
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Best Local
W09718838-A1
                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                        Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                          Region
                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                        Chimeric
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                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                  acute leukocyte mediated lung injury; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22419 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cystic tumours.
See also AAR60626.
                                     Region
                                                                Region
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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les 118; Conserv
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                                                                                                                                                                                                                                                                               synthetic.
                                                                                                                                                                                                                                                                                                  Mus musculus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                  109.
                                     /label= CDR3
/note= "21.6 complementarity determining
117..126
                                                                                   /label= FR3
                                                                                                   /label= CDR2
/note= "21.6
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                       'note= "REI framework region
                                                                                                                              'note= "REI framework region
                                                                                                                                         'label= FR2
                                                                                                                                                         /note= "21.6 complementarity determining
                                                                                                                                                                    /label= CDR1
                                                                                                                                                                                    /note= "REI framework region
                                                                                                                                                                                                              /label= Mat_protein
/note= "VL version La (Claim 25)"
                                                                                                                                                                                               'label= FR1
                                                                                                                                                                                                                                            'label- Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%;
93.7%;
                                                                .116
                 framework region 4"
                                                                                                 complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 634; DB 15;
Pred. No. 5.9e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                            region
                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                          1,
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                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                     AAR06252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VH (see AAW22413) can be use to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions from the VL region (see AAW22409) of mouse alpha-4 integrin monocional antibody 21.6 and a modified human REI framework. It can be antibody 21.6 and a modified human REI framework.
                            EP380068-A.
                                                                                       Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                       Variable region of murine AHT
                                                                                                                                                       10-DEC-1990
                                                                                                                                                                                      AAR06252;
                                                                                                                                                                                                                 AAR06252 standard; protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uses of humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in mammalian host cells following PCR amplification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 10; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1997
                                                                                                                                                                                                                                                                                                                                121 TKLEIK 126
                                                                                                                                                                                                                                                                                                121 tkveik 126
                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                          gkaprllihytsalqpgipsrfsgsgsgrdytftisslqpediatyyclqydnlwtfgqg 120
                                                                                                                                                                                                                                                                                                                                                                              GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones ST,
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.0%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leger OJ, Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 619; DB 18;
Pred. No. 9.2e-43;
                                                                                                                    107 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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01-AUG-1990

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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1989;
24-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vectors for producing chimeric monoclonal antibodies which express human constant region and non-human variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-232892/31.
N-PSDB; AAQ05556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zerler B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-1990;
                                                                                                                                                                 antibody engineering.
                                                                                                                                                                                                               02-APR-1996
                                                                                                                                                                                                                                                   AAR81328 standard; Protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; ; p; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR THERAPEU
                                                                                 Region
                                                                                                                                                Mus musculus
                                                                                                                                                                          Humanized antibody; leukocyte
                                                                                                                                                                                                                                AAR81328;
        Regior
                                            Region
                                                                                                                    Region
                                                                                                                                                                                            Mouse anti-VLA-4 antibody 21.6 light chain variable region
                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                               121 gtklevr 127
                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                 GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 88.1
112; Conservative
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0441702
89US-0301216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90EP-0101351
50..56
/label= CDR2
                                             35..49
                          /note=
                                    /label=
                                                              /note=
                                                                         -Tabet
                                                                                                   /note=
                                                                                                             /label= FR1
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   91.0%;
88.2%;
                   "mouse light chain region 2"
                                                    "mouse light chain variable determining region 1"
                                                                                          "mouse light chain variable framework region 1" \,
                                    FR2
                                                                        CDR1
                  region
                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 618.5; DB Pred. No. 1e-42; Mismatches
                                                                                                                                                                          adhesion molecule; VLA-4; therapeutic;
                           variable
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
                                                             complementarity
                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           1;
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RESULT
AAY29913
ID AAY2

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AAY29913 standard;

Protein;

359

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B QY Db 9

61

81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126

0;

rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106

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Query Match
Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                               chain. Plasmids encoding the chimeric antibodies are transfected into COscells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LCVR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                            anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-269276/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                    21
                                                                                                        Local Similarity
nes 106; Conserv
1 digmtgspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips
                           DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM,
                                                                                                                                                                                                                                       106 AA;
                                                                                                   83.7%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0186269
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/label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89..96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "mouse light chain variable framework
    region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mouse light chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mouse light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mouse light chain variable
region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
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                                                                                                        0;
                                                                                                        Score 569; DB 16
Pred. No. 8e-39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain variable region 3"
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                                                                                                                                                          16;
                                                                                                           0,
                                                                                                                                                          Length 106;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementarity
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     DY XX
                                                                                        AAY29911
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV pp120; (6) human SDF-1 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or proventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of fumour antigen epitopes. The present sequence represents a fusion protein from the present invantion
17-NOV-1999 (first entry)
                                    AA $29911;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 118-119; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9946392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                      AAY29911 standard; Protein; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MCP-3 and murine scFv38 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY29913;
                                                                                                                                                           289
                                                                                                                                                                                                                             229
                                                                                                                                                                                     77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                           17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                         9
                                                                                                                                                    gipsrfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338
                                                                                                                                                                                                                     gsgsdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biragyn A;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0077745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US05345
                                                                                                                                                                                                                                                                                                            79.3%;
                                                                                                                                                                                                                                                                                            Score 539; DB 20;
Pred. No. 6.7e-36;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                             Length 359;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          0;
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AAY29916
                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and HIV gp120; (7) human MDC and HIV gp120; and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes and fine mapping of temporary incompletions.
                                                         Artificial synthetic construct protein SEQ ID NO:15.
                                                                                                                      17-NOV-1999
                                                                                                                                                                             AAY29916;
                                                                                                                                                                                                                              AAY29916 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 115-116; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion polypeptides comprising a chemokine and a tumour antigen HIV antigen, used for treating cancers or treating or preventing HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551418/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09946392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%;
91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 539; DB 20; Pred. No. 6.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion polypeptides comprising a chemokine and a tumour antigen ( {\rm HIV} antigen, used for treating cancers or treating or preventing {\rm HIV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 117-118; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-551418/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                    Synthetic
                                                     Monoclonal antibody; heavy metal; mercury; variable region;
                                                                          Light chain variable region for monoclonal antibody 23F8.
                                                                                                 21-DEC-1995
                                                                                                                        AAR78970
                                                                                                                                             AAR78970 standard; Protein; 107 AA
                                                                                                                                                                                                    155 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 200
                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                               21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes fusion proteins comprising a chema tumour antigen or HIV antigen. Specifically claimed fusion
                                                                                                                                                                                                                                                                                                                                                                         not mentioned further within the specification.
                                                                                                                                                                                                                                                                                               100;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0077745
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                                                                                                                                                                                                                                                                                                        78.78;
94.38;
                                                                                                                                                                                                                                                                                                        Score 535; DB 20;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                  Length 374;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a chemokine
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                               Gaps
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 antibody engineering
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She and 3EB) were producing MADS that were strongly positive against glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MALLY reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5° end of the CHI domain of the 5° and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAO97511-097518. The primer used for cDNA synthesis are variable region of a particular antibody polypeptide was also used for cPR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAO97518 was used to amplify the mAD 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAO97498-097510 and the deduced AA sequences in AAR97941-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridoma antibodies have been produced with the spleen cells of BALB/C mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2Dings, KLH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 67-68; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neutralising heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-275415/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                        Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
                                                                                                                                          02-APR-1996
                                                                                                                                                                                                            AAR81321;
                                                                                                                                                                                                                                                                                 AAR81321 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ97508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.1%; Score 510.5; DB 16; 91.6%; Pred. No. 4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23F8, 2D5
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RESULT 1
AAW22412
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ends of the mouse cDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies cell and for inhibiting adhesion of a leukocyte to an endothelial sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can be used for detecting VLA-4, for affinity purification or for
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                      08-DEC-1997 (first entry)
                                                                                                                                                                                       AAW22412 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3'
                                                                                   Humanised alpha-4 integrin antibody 21.6 VL La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09519790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Mus musculus.
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1995
                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                              21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                               1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%;
88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 508; DB 16;
Pred. No. 6.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                      6;
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                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Claim 25; Fig 6; 107pp; English.
                      asthma, atherosclerosis, AIDS,
                                 Uses of humanised alpha-4 integrin antibody -
                                                                                   Bendig MM,
                                                                                                                                                       21-NOV-1996;
                                                          WPI; 1997-297879/27
                                                                                                         (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                  21-NOV-1995;
                                                                                                                                                                               29-may-1997.
                                                                                                                                                                                                      WO9718838-A1
                                                                                                                                                                                                                                                   Misc-difference 106
                                                                                                                                                                                                                                                                                     Misc-difference 104
                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                             Region
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Chimeric Homo sapiens;
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                                                                                   Jones ST,
                                                                                                                                95US-0561521
                                                                                                                                                       96WO-US18807
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                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                          /note= "REI Leu-103 substd. by Val,
                                                                                                                                                                                                                                                                                                                                                                 /label= CDR3
/note= "21.6 complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                             89..96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "21.6 complementarity determining region 2" 57..88
                                                                                                                                                                                                                                                                                                                                                /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "REI Val-58 is substd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "21.6 complementarity determining region 1" 35...49
                                                                                                                                                                                                                                                                                                                                 /note= "REI framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "REI Lys-45 is substd. by Lys of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "REI framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= FR1
                                                                                Leger OJ,
                                                                                                                                                                                                                       "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                        "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                       "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                                              of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VL, important in supporting the loop "
                         dementia, etc
                                                                                Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by Ile of mouse
                                 for treatment of
                                                                                 Yednock TA;
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AAR93159
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour
                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                         Antibody; light chain; kappa; variable region; K20; integrin; CD29;
beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                           T cell activation;
                                                                                                                                                                                                                                                                                                                                                                                                                       Murine monoclonal antibody K20 kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1996
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                                                                                                      /note=
57..88
                                                                                                                                                                                           /note=
35..49
               /note= "complementarity determining region"
95...108
                                                            /note= "framework region"
89..94
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                               /note= "framework region
/label= J_kappal
                                                                                       /label= fR3
                                                                                                                                    /label= CDR2
                                                                                                                                                                                /label= FR2
                                                                                                                                                                                                                           /label= CDR1
                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                           complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%;
88.7%;
                                                                                                                    "complementarity determining
                                                                                                                                                                                                          "complementarity determining region"
                                                                                                                                                                                                                                                      "framework region"
                                                                                                                                                                                                                                                                      FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 508;
Pred. No. (
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S X C C C C C C C C C C C X P X P T T X R X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 2A; 39pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanisation of non-human immunoglobulin variable regions - prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT26849
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                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR26983 standard; Protein; 637
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                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                      Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2; variable region; ETA.
                                                                                                                                                                                                                                                                                                                                                                         (FRP51)-ETA fusion protein
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                                                                                   Peptide
                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                       Location/Qualifiers
                                                                                                              /label=
                                                     /label= FLAG_peptide_and_enterokinase_cleavage_site
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89.6%;
FWP51_heavy_chain_variable_domain
                                                                                                              ompA_signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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Pred. No. 6.4e-34;
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Best Local Similarity
                                                                                                                                                                                                                                            The sequences given in AAR26982-3 contain part of the exotoxin A (ETA) sequence corresponding to positions 252-613 of the full exotoxin A sequence. These sequences are encoded by FV(FRP5)-ETA fusion genes. The ETA sequence was used as a marker gene so that E. coli transformed with the fusion gene could be identified. The fusion genes were expressed in E. coli and the antibodies were extracted. These recombinant antibodies can be used for the qualitative and quantitative determination of c-erbB-2. This can be used for monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 53-58; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant antibodies directed to growth factor receptor C-erbB-2 for diagnosing and treating tumours expressing C-erbB-2 e.g. breast or ovarian tumours \,
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Zwickl M;
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US-08-561-521-2 US-08-561-521-2 US-08-561-521-2 Sequence 2, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION: APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Saldanha, Jose APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran ITILE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend khourie and Crew STREET: One Market plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94105 COMPUTER RADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy Misk COMPUTER PALDABLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER SALDABLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER RADABLE FORM: APPLICATION NUMBER: US/08/561,521 FILING DATE: CLASSIFICATION LATA: APPLICATION NUMBER: US/08/561,521 FILING DATE: 25-JAN-1994 ATTORREY/AGENT INFORMATION: NAME: Smith, William L NAME: Sm	28 426.5 62.7 127 2 US-08-436-717-37 29 424.5 62.4 127 3 US-08-649-100-17 30 423.5 62.3 236 1 US-08-579-940-2 31 418.5 61.5 142 2 US-08-879-940-2 32 418.5 61.5 142 4 US-08-838-992-4 417.5 61.4 127 1 US-08-137-117D-29 34 417.5 61.4 127 1 US-08-137-117D-29 35 417.5 61.4 127 3 US-08-933-983-7 36 416.5 61.2 127 2 US-08-621-751A-6 416.5 61.2 127 2 US-08-621-751A-6 39 413.5 60.8 125 2 US-08-470-139-26 41 413.5 60.8 125 2 US-08-470-139-26 42 413.5 60.8 125 2 US-08-489-109-3 43 412.5 60.8 125 2 US-08-489-100-3 43 410.5 60.4 127 3 US-08-465-313-2 42 413.5 60.8 125 2 US-08-465-313-2 43 410.5 60.4 128 4 US-09-136-315-8 44 410.5 60.4 128 4 US-09-33-983-17 45 410.5 60.4 128 4 US-08-59-147-80
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT Saldanha, Jose APPLICANT: Jones, S. Tarran
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                        61 GKRPRLLIHYTSALQPGIPSRFSGSGSGNYSFNISNLEPEDIATYYCLQYDNLWTFGGG
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                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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STATE: California
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Sequence 15, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
                                                       PCT-US95-01219-15
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                                                                                                                                                                                                                                                                                 В
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 2:
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
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                                                                                                                                  121 TKLEIK 126
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94105
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STATE: California
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Jones, S. Tarran
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TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                     / Match 100.0%; Score 680; DB 5; Local Similarity 100.0%; Pred. No. 1.3e-59; nes 126; Conservative 0; Mismatches 0;
61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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                                                                                                                            1 MRPSTQFLGLLLFWLHGAQCDTQMTQSPSSLSASLGGKVTTTCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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Best Local (
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APPLICATION NUMBER: US 08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
                                                                                                                                         APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

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CITY: San Francisco
STATE: California
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LENGTH: 126 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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CORRESPONDENCE ADDRESS:
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    STREET: P.C.
STREET: P.C.
STREET: 5558f
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                                                                                                                     ADDRESSEE:
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Similarity 100.0%; Pred. No. 1.3e-59;
26; Conservative 0; Mismatches 0;
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No. 5558852th Carolina
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                                                                                    P.O. Drawer 34009
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Saldanha, Jose
Jones, S. Tarran
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                                                                                                                         Kenneth D.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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APPLICATION NUMBER: US 01
FILING DATE: 19-MAR-1993
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION: 919-420-2200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                     TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                               ZIP:
                                                                                                                                                COUNTRY:
                                                                                                                                                                  STATE:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/339,582
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118;
                                                                                                                                                                                   San Francisco
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                                                                                                                               94105
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                                                                                                                                                                  California
                                                                                                                                                                                                    One Market Plaza, Steuart Tower, Suite 2000
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93.7%;
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US/08/561,521
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Pred. No. 4.2e-55;
3; Mismatches 5
                                        Version #1.25
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 5:
                  TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/01219 FILING DATE: 25-JAN-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPERATOR STORMERS PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                            REFERENCE/DOCKET NUMBER:
                                                                                            REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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CLASSIFICATION:
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Smith, William L.
Smith, William L.
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100.0%; Pred. No. 7.6e-49;
                                                                                                                                                                    US 08/186,269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22,
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Best Local Similarity
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                                                                                  TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                  SEQUENCE CHARACTERISTICS LENGTH: 107 amino acid
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07

FILTUR DAMP
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NAMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercur
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                      REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               FILING DATE: 14-MAR-1989 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 14-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: >0 ___CTTY: Minneapolis
                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                107 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Merchant & Gould
90 South 7th Street, 3100 No. 5972656west Ctr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                linear
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03-JUL-1997
                                                                                                                                                                                              Charles
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                                                                                                                                                                                                                                                  US 07/324,392
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                                                                                                                               Query Match
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APPLICANT:
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
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                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 75.1%;
Local Similarity 91.6%;
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                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                              21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                              Local
                                                                                                                                                                                                                                                             LENGTH:
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RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                              Similarity
                                                                                                                                                                                                                                             amino acid
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                             106 amino acids
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Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig, Mary M.
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                              protein
                                                                                                                                                                                                                            single
                                                                                                            74.7%;
88.7%;
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                                                                                                                                                                                                                                                                                                                                                                           30,223
                                                                                             Score 508; DB 2; Length 106; Pred. No. 7e-43; 6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                             15270-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 510.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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RESULT 11
US-08-235-838-16
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                                                                       Patent No. 5571894
GENERAL INFORMATION:
                                                                                            Sequence 16, Application US/08235838 Patent No. 5571894
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08 FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
 APPLICANT:
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                                                                                                                                                                                                                                                                                                    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                            81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                   Wels, Winfried S. Hynes, Nancy E. Harwerth, Ina-Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones, S. Tarran
Groner, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
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88.7%;
                     Ina-Maria
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                                                                                                                                                                                                                                                                                                                                                                       Score 508; DB 5
Pred. No. 7e-43;
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                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 106;
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                                                                                                                                                                                                                                                         Sequence 16, Application US/08465473B Patent No. 5939531
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                                                                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
                  NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
                                                                             APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                         APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina Maria
APPLICANT: Groner, Bernd
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/828,832 FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                          224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223
                                                                                                                                                                                                                                                                                                                                                                                                               77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/235,838
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      564 Morris Avenue
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nilarity 86.4%;
Conservative
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                                                                                                    Recombinant Antibodies Specific
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US-08-235-838-11
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GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
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TELEPHONE: (908)522 6940
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                                                                                                                                                                                                    STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / STREET: / STREET: / STREET: / STREET: / STREET: / L. STREET: / STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / L. STREET: / 
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palantin
COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                           COUNTRY:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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)GY: linear
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   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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5 June 1995
N. 425
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Pred. No. 5.8e-42;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-838-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08465473B Patent No. 5939531
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Mari
APPLICANT: Groner, Bernd
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APPLICATION NUMBER: GB 9
FILING DATE: 05-FEB-1991
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STREET: JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU JUNEAU J
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OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
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REGISTRATION NUMBER: 36,
                                  APPLICATION NUMBER:
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31-JAN-1992
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86.2%;
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                               US 07/828,832
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                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19 FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21 FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
TELEFAX: (
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT:
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TELEPHONE: (908)522 6940
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ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                        TELEPHONE:
                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
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nes 94; Conserv
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Boque, Lluis
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         2: (415) 576-0200
(415) 576-0300
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IVENTION: Recombinant Ribonuclease Proteins
SOUENCES: 64
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ER: 4-18518/A/CIP/CONT2
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Pred. No. 5.7e-42;
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

## 19 Rappa chain - mouse (fragment) 12 Rappa chain - mouse (fragment) C:Species: Mus musculus (house mouse) C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000 C:Accession: S09365 R;Feddersen, R.; van Ness, B. Nucleic Acids Res. 17, 9797-9809, 1989 Nucleic Acids Res. 17, 9797-9809, 1989 A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobul A; Reference number: S09365; MUID:90098844 A;Accession: S09365 C:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM> A;Status: preliminary A;Molecule type: DNA A;Residues: 1-125 <FED> of kappa immunoglobulin gene

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02222	D D G G	C C C H S R	Дb	Qy	Qy Db	Оу Об	
A; Ktatus: preliminary A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-104 <sta> A; Cross-references: EMBL: X59185; NID: g52316; PIDN: CAA41895.1; PID: g1334063 C; Superfamily: immunoglobulin V region; immunoglobulin homology</sta>	R;Stark, S.E.; Caton, A.J.  J. Exp. Med. 174, 613-624, 1991  J. Exp. Med. 174, 613-624, 1991  A;Title: Antibodies that are specific for a single amino acid interchange in a A;Reference number: S26309; MUID:91341421  A.Accession: S26330	RESULT 2  \$26330  Ig kappa chain V region - mouse  C;Species: Mus musculus (house mouse)  C;Species: 13-Jan-1995 #text_change 20-Jun-2000  C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000  C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000	118	120			Query Match Best Local Similarity 90.6 Matches 115; Conservative
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A;Cross references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189 C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                            A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
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A; Residues: 1-104 <STA>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
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J. Exp. Med. 1
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F; 16-90/Domain: immunoglobulin homology <IMM>
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Best Local :
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                                                                                                                                                                                                                                                                                                                  k, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104
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Local Similarity 95.2%;
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174, 613-624, 1991
           Conservative
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                            91.5%;
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                      Score 524; DB 2;
Pred. No. 1.6e-38;
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        Mismatches
                                            Length 106;
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A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-103 <STA> A;Residues: 1-103 <STA> A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064 A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sea A;Accession: S26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Antibodies that are specific for a single amino acid interchange in A;Reference number: S26309; MUID:91341421
A;Accession: S26332
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                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-103 <ST2>
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A; Residues: 1-103 <ST
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J. Exp. Med. 174, 613-624, 1991
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Ig light chain V region - mouse (fragment)
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C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy L.; Der submitted to the EMBL Data Library, March 1995
submitted to the EMBL Data Library, March 1995
submitted to the EMBL Data Library, March 1995
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A; Residues: 1-129 < ROC>
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A; Accession: S52789
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Pred. No. 1.5e-35
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R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444

A;Accession: PH1064

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                        R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325
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                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-94 <LAW>
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                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                            21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                     Local Similarity
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90;
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87.4%;
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93.8%;
                                                                                                                  70.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 488; DB 2;
Pred. No. 1.9e-35;
                                                                                                                  Score 476; DB 2;
Pred. No. 1.9e-34;
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                                                                                               Mismatches
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                                                                                                                                           Length 94;
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C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
J. Exp. Med. 171, 265-297 autoimmune mice arise by clonal expansion and somat A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-23/Region: framework 1
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
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A; Residues: 1-107 <SHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
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F;98-107/Region: framework 4
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                                                                                                                                                                                                                                                                                                                             A;Molecule type; mRNA
A;Res!dues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: PL0231; MUID:90111618 A; Accession: PL0272
                                                                                                                     F;57-88/Region: f
F;89-97/Region: c
F;98-107/Region:
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  91;
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                                                                                                                                                  complementarity-determining
                                                                                                                                                                               framework 3
                                                                                                                                                                                                     complementarity-determining
                                                                                                                                                                                                                                                                             immunoglobulin homology <IMM>
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Conservative
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86.0%;
                       68.5%;
85.0%;
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  5; Mismatches
                          Score 465.5;
Pred. No. 1.8
                             1.8e-33;
                                                  DB 2;
     10;
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F;50-56/Region: cc
F;57-88/Region: f;
F;89-97/Region: cc
F;98-107/Region:
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A;Accession: PLO271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-23/Region: framework r
F;14-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;35-49/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Speciles: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
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F; 35-49/Region: framework 2
F; 50-56/Region: complementarity-determining 2
F; 57-88/Region: framework 3
F; 69-97/Region: complementarity-determining 3
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
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A; Residues: 1-107 <SHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS
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                                                                                                   complementarity-determining
                                                                                                                                  framework 3
                                                                                                                                                  complementarity-determining 2
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     68.3%;
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     Score 464.5;
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Pred. No. 2.2e-33;
  DB
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  2
Length 107;
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A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                               C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Reur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes
                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar_1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-132 <KLE>
                                                                                                                                                                                                                                        A:Status: preliminary; translation not shown
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                        A; Accession: S40334
                                                                                                                                                                                                                                                                                           A; Reference number: S40312; MUID:94080891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-127 < KLE>
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Best Local
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Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKDGKRPR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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      Conservative
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65.5%; Score 445.5;
64.6%; Pred. No. 1.1;
tive 21; Mismatches
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ches 11;
                         .1e-31
                                         DB 2;
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Ig Rappa chain - human .

C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891
A;Recession: $40365
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:9441418; PIDN:CAA51143.1; PID:9441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
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S40365
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Search completed: May 7, 2002, 12:23:47 Job time: 198 sec
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62 GKAPKLLIYVASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGG 121
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Maximum Match 100%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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P01639
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P0161595
P01595
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                                    P01598
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P01643
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   musculu
no sapien
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

IG KAPPA CHAIN V-I REGION WALKER

FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY. COMPLEMENTARITY-DETERMINING SIGNAL CHAIN

Immunoglobulin

V region;

Q

1 MRPSIQELGLLLFWLHGAQCDIQMIQSPSSLSASLGGKVTITCKTSQDINKYMAMYQHKP 60

Query Match
Best Local Similarity 66.9

64.9%;

Length Indels

129; سو --Gaps

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15; Mismatches Score 441.5; DB 1; Pred. No. 5.2e-38; 5; Mismatches 26; DISULFID NON\_TER SEQUENCE

129 129 AA;

14069 MW;

F941FA07D4AFC2F9 CRC64;

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RESULT 2
KV5E_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altenburger W., Steinmetz M., Zachau H.G.; "Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma."; Nature 287:603-607(1980).
      120 GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01920; KVMST1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V00772; CAA24150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=81052342; PubMed=6776411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV5E_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                               61 GKSPKTLLYRANRLVDGVPSRFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGA 120
                                                         61.GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 GTRLEIK 129
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                                                                                                                                                                    Local Similarity
                                                                                                                 1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-V REGION T1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                       MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRVPAQLLGLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP 62
                                                                                                                                                     Conservative
                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                               V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                      43
54
69
76
108
117
127
108
                                                                                                                                                                62.6%;
62.2%;
                                                                                                                                                                                                                          14385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                     18;
                                                                                                                                                              Score 425.5; DB 1
Pred. No. 2.2e-36;
                                                                                                                                                                                                                                                                                                       FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                FRAMEWORK
                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-V REGION T1. FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                       AFA5563D31BB7E05 CRC64;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AA.
                                                                                                                                                                             DB 1;
                                                                                                                                                  29;
                                                                                                                                                  Indels
                                                                                                                                                                            Length 128;
                                                                                                                                             Gaps
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RESULT 4
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Query Match
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV1X_HUMAN STANDARD; PRT; 129 AA P04432; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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123 GTKVDNK 129
                                  120 GTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006;
InterPro; IPR003596;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X00966; CAA25478.1; ALT_TERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=85014148; PubMed=6091049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 12:6995-7006(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klobeck H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                   63 GKAPTILIYAVSNLQVGVPSRFSGSGSGAEFTLTISSLQPEDFATYYCQQNYNFSFTFGG 122
                                                                                           61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin genes of the kappa light chain type from two human ymphoid cell lines are closely related.";
                                                                                                                                                                                            1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                    MRVPAQLLGLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKP 62
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
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45
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129
                                                                                                                                                                                                                                                                                                                                              14235 MW;
                                                                                                                                                                                                                                                               60.7%;
61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                             Score 412.5;
Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK 4
BY SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG KAPPA CHAIN V-I REGION DAUDI
                                                                                                                                                                                                                                                                                                                                              CAF076BC7E5574C8 CRC64;
                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                               4.5e-35
                                                                                                                                                                                                                                                                                 DB 1;
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P01602;
P01602;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-I REGION HK102 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes_and_a_pseudogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-81098966; PubMed=6779204;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMARR; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00245; AAA59087.1; -.
EMBL; Z00001; CAA77292.1; -.
PIR; A01882; K1HU12.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley D.L., Rabbitts T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                   MOUSE
     NCBI_TaxID=10090;
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                          61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRPSIQELGLLLEWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
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                                                                                               KAPPA CHAIN V-V REGION L6 PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                 GKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                           288:730-733(1980)
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Pred. No. 4.7e-34;
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COMPLEMENTARITY-DETERMINING 1.
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Best Local
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"Differences between germ-line and rearranged immunoglobulin V kappa
coding sequences suggest a localized mutation mechanism.";
Nature 291:668-679(1981).
PIR; A01921; KYMSL5.
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SEQUENCE FROM N.A.
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                               Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E., Schwager P., Steigemann W., Schramm H.J., The structure determination of the variable portion of the
                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin L-chain of the kappa-type, protein Au). ";
                                                                                                                     Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-i- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED
                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY.
MEDLINE=77022433; PubMed=1234024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    REGION OF THE KAPPA CHAIN REI.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                               Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
                                                                                                                                                                                                                                                                                                                                                                                                   Table of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=72189444; PubMed=5028201; Schiechl H., Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                MOLECULAR REPLACEMENT METHODS USING
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  A01862; K1HUAU
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Pred. No. 7.4e-34
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PIR; A01873; KIHURE.
PDB; 1REI; 17-FEB-84.
InterPro; IPR003006; Ig_wHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN 23 FRAMEWORK 1.
DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                    MEDLINE-76039968; pubMed-1182131; Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.; "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution."; Biochemistry 14:4943-4952(1975).
                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE-76039968; PubMed=1182131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01607;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                    kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
                                                                                                                                                                                                                                                                                                      three-dimensional structure of antibodies, in particular their
                                                                                                                                                                                                                                                                                                                                                         "The primary structure of a crystalline monoclonal immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                Palm W., Hilschmann N.;
                                                                                                                                        !- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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1 23 FRAMEWORK 1.
2 COMPLEMENTARITY-DETERMINING
5 49 FRAMEWORK 2.
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Pred. No. 1.2e-33;
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                                                 Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.; (In) Franek F., Shugar D. (eds.);
          -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
                                    Gamma globulins: structure and function, pp.57-74, Academic Press New York (1969).
                                                                                                                                                                                    KVIP_HUMAN STANDARD; PRT; 108 AA P01608; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat. IG KAPPA CHAIN V-I REGION ROY.
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                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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SEQUENCE
                          -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                              REVISIONS TO 39 AND 41.
                                                                                            Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
                                                                                                           "Chemical structure of 2 kappa-type Bence Jones proteins
                                                                                                                         Hilschmann
                                                                                                                               MEDLINE=68362076; PubMed=5595110;
                                                                                                                                          SEQUENCE
                                                                                                                                                        NCBI_TaxID=9606;
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      A01874; K1HURY
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                                                                                                                                                             Catarrhini; Hominidae; Homo
                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M., Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV1Y_HUMAN
                                                                                                                                                                                                                                                          "Characterization and preliminary crystallographic data on the VL-
related fragment of the human kI Bence Jones protein Wat.";
J. MOI. Biol. 147:185-193(1981)
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PDB; INTL: 01-NOV-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 33:14848-14857(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                    Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81267384; PubMed=6167731;
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                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region
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68.2%;
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COMPLEMENTARITY-DETERMINING 3.
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COMPLEMENTARITY-DETERMINING
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                                                                                         COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
       FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
                                                                      COMPLEMENTARITY-DETERMINING
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RESULT 10
KV1A_HUMAN
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"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

J. Biol. Chem. 244:3550-3560(1969).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                     DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV1A_HUMAN
                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; SMART; SM00406; IG;
                                                                                                                                                                                                                                                                                                                                                                   PIR; A01861; K1HUAG. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-I REGION AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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InterPro; IPR003596; Ig_v.
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                                 61
                                                     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                           21 DIOMTOSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
11
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                                                                              DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60
                                 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107
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IGv; 1.
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67.3%;
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69.2%;
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                                                                                                                                         Score 380.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                       FRAMEWORK
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                                                                                                                                                                                         E3B3B246C18F0C4F CRC64;
                                                                                                                                Mismatches
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                                                                                                                                          6.5e-32;
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Best Local :
                                                                                                                          KYG_MOUSE STANDARD; PRT; 130 AA. P01639; P01640; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 16 KAPPA CHAIN V-V REGION MOPC 41 PRECURSOR.
"A kappa:immunoglobulin gene is formed by site-specific recombination
                  MEDLINE=79221900; PubMed=1111146; Seidman J.G., Max E.E., Leder P.;
                                                SEQUENCE FROM N.A.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID NON_TER
                                                                           NCBI_TaxID=10090;
                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scand. J. Immunol. 5:677-684(1976).

-1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN. WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete amino acid sequence of the variable domains of two IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra J.D., Klap
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION LAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                               61 RESGSGSGTDFTETISSLQPEDIATYYCQQYNN-WPPTEGQGTKVEVK 107
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                                                                                                                                                                                                                                                                                        RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                  DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
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11834 MW;
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Pred. No. 8.2e-32;
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BY SIMILAR
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COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1
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                                                                                P06313;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MEDLINE=86041853; PubMed=2997712;
             SEQUENCE FROM N.A
                                      NCBI_TaxID=9606;
                                                                          Homo sapiens (Human)
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SEQUENCE
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VARIANT
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01922; KVMSM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kappa chains.";
Science 155:465-467(1967).
-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **Burstein Y., Schechter I.; ***Maino acid sequence of the NH2-terminal extra piece segments of the Precursors of mouse immunoglobulin lambdal-type and kappa-type light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin V region; Signal; Bence-Jones protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=67056897; PubMed=4162931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   without further somatic mutation.";
Nature 280:370-375(1979).
[2]
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MEDLINE=77148916; PubMed=403522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rray W.R., Dreyer W.J., Hood L.;
Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
                                                                                                                                                                                                                                                            63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG
                                                                                                                                                                                                                                                                                                                                    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                          MRAPAQIFGFLLLLFQGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP 62
                                                                                                                                                                                                                                          GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA;
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129
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59.1%;
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MISSING (IN 25% OF THE MOLECULES).
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Nucleic Acids Res. 13:6515-6529(1985).
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kappa genes and a pseudogene.";
Nature 288:730-733(1980).
[2]
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION HK101 PRECURSOR (FRAGMENT).
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                                                                                               Bentley D.L., Rabbitts T.H.;
                                                                                                                   SEQUENCE FROM N.A. MEDLINE=81098966; PubMed=6779204;
                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                         KV1I_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                   'Human immunoglobulin variable region
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IPR003596; Ig_v.
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Best Local
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InterPro; IPR003596; Iq
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1
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Bentley D.L., Rabbitts T.H.;

"Evolution of immunoglobulin V genes: evidence indicating
"Evolution of immunoglobulin V kappa sequences have diverged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.lsb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A21056; A21056.
HSSP; P01607; 1REI.
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EMBL; K01324; AAA58932.1; -.
EMBL; V00558; CAA23824.1; -.
PIR; A01881; K1H111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 32:181-189(1983).
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                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-V REGION MOPC 173.
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                      "Determination of the primary structure of immunoglobulin. Amino-acid sequence of the Eur. J. Biochem. 59:525-537(1975).
                                                                                   Schiff C., Fougereau M.;
                                                                                                              MEDLINE=76091934; PubMed=812696;
                                                                                                                                      SEQUENCE
                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                        P01643;
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- |- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP
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                                                                                                                                                                                                         Eutheria;
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                                                                                                                                                                                                           Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 378; DB 1, Pred. No. 1.3e-3;
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                             sciurognathi;
                                                                                                                                                                                                                                 Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D7D0FF3718CEF587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   108
                                              the light
                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                Muridae;
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                                                                       mouse IgG2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                   chain.";
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DR PIR; A01926; KVMS73.

DR InterPro; IPR003596; Ig_W.

DR InterPro; IPR003596; Ig_V.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; 1g; 1.

EN SMART; SM00406; IGV; 1.

KW Immunoglobulin V region.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 49 FRAMEWORK 2.

FT DOMAIN 57 88 FRAMEWORK 3.

FT DOMAIN 98 108 FRAMEWORK 4.

FT DOMAIN 98 108 FRAMEWORK 4.

FT DOMAIN 98 108 BY SIMILARITY.

FT DOMAIN 189 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 98 108 FRAMEWORK 4.

FT DOMAIN 189 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 189 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 189 97 COMPLEMENTARITY.

FT DOMAIN 189 108 FRAMEWORK 4.

FT DOMAIN 189 108 FRAMEWORK 3.

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Search completed: May 7, 2002, 12:32:34 Job time: 565 sec

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OM protein - protein search, using sw model
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Perfect score:
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1: sp_archea:*
2: sp_bacteria
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Gapop 10.0 , Gapext 0.5
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                                                                                  sp_organelle:*
sp_phage:*
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sp_vertebrate:*
sp_unclassified:*
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                                                sp_rodent:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	&	7	6	υī	4	ω	N	ᆫ	Result No.
281.5	288.5	289.5	291.5	292.5	295.5	299	305.5	308	310	317.5	319	341.5	346.5	362	372.5	378.5	380.5	389.5	Score
41.4	42.4	42.6	42.9	43.0	43.5	44.0	44.9	45.3	45.6	46.7	46.9	50.2	51.0	53.2	54.8	55.7	56.0	57.3	Query Match L
114	99	103	97	101	107	106	108	109	109	238	109	298	108	107	107	108	214	108	Length
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Q9UL80	Q9JL74	Q9JL80	Q9JL76	Q9JL78	Q9ERZ9	Q9U410	Q9UL83	Q9UL86	Q9UL85	Q99M37	Q9UL78	Q9QYF0	Q9UL79	Q9UL81	Q9JL84	Q9UL70	Q9R1A5	Q9UL77	ID
Q9u180 homo sapien	Q9j174 mus musculu	Q9j180 mus musculu		Q9j178 mus musculu	Q9erz9 mus muscuiu	Q9u410 schistosoma	Q9ul83 homo sapien					Q9qyt0 mus muscuiu			Q9j184 mus musculu		Q9rlab mus musculu	Q9u177 homo sapien	Description

23 204.5 24 193.5 25 188.5 26 185 27 140.5 29 140.5 29 110 30 124 31 124 32 119 33 118.5 35 117 36 117 37 116.5 38 115.5 39 115.5 39 115.5 39 115.5 31 115.5 31 115.5 31 115.5 32 110.5	20 262 21 252.5 22 209
5 28.5 5 28.5 5 27.2 5 27.2 5 20.6 9 19.0 10.5 117.5 117.2 117.2 117.2 117.2 118.2 119.0 117.2 117.2 117.2 117.2 118.2 119.0 119.	
107 235 235 235 3109 3109 337 100 169 509 509 509 509 509 509 509 509 509 50	104 109 107
11444 1111 111444 1111 1111 1111	11 6
Q9UL22 Q9UP22 Q9UP11 Q9E713 Q9E713 Q9E71624 Q9H524 Q9Y2N4 Q9Y2N6	Q9JL82 Q9N0W5 Q9NSD6
Ogula homo sapien Ogunza homo sapien Ogunza mus musculu Ogunza mus musculu Ogunza mus musculu Ogunza mus musculu Ogunza mus musculu Ogunza homo sapien Ogyza mus musculu P97710 rattus norv P97710 rattus norv P97797 mus musculu P97797 mus musculu P97797 mus musculu O70426 rattus norv P78324 homo sapien Ogyka mus musculu O08907 mus musculu O091005 sphoeroides Oghlu5 homo sapien Ogy4v0 homo sapien Ogy4v0 homo sapien Ogy4v0 homo sapien Ogy4v0 homo sapien	

## ALIGNMENTS

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Q9UL77;
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
pfam; pF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON TER 1
                                                                                                                                                                                                                                                                              EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                            Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive autoantibodies in rheumatic carditis and normal
81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
                                                            21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                          Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                        108 AA;
                                                                                                                                                                                         108
                                                                                          57.3%; Score 389.5; DB 4; Length 108; ilarity 68.2%; Pred. No. 5.6e-35; Conservative 13; Mismatches 20; Indels 1
                                                                                                                                                                        11738 MW; C06681716C4D16F3 CRC64;
                                                                                                1; Gaps
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RESULT
Q9UL70
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Best Local
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                                                    SEQUENCE FROM N.A.

MEDLINE-98277139; Pubmed-9614934;

Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                         01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                  Clin.
                           fetus.";
                                                                                                  NCBI_TaxID=9606
                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                           Q9UL70;
                                                                                                                                                                                                      Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scry).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
     -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF152371; AAD40242.1; -. HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9R1A5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                              DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
                                                                                                                                                                                                                                                                                                                   DIOMTOSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                     RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
              Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                    214
23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                       56.0%;
                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                       P.L., Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                      Score 380.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                   108 AA
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                                                                                                                                                                                                                                                                                                                                                       1.2e-33
                                                                                                             Hominidae;
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Q9UL81;
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                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JL84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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HSSP; P01607; 11
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                                                                                                                                                              Local
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                               σ
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                            Similarity
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                                                                                                                                                                                                       107 AA;
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Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF206022; AAF69320.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003596;
                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                         21 DIQMTQSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                 1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                   RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
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  PRELIMINARY;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD56280.1;
                                                                                                                                                                                                                                                                                                                                                                                107
11648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                              54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                            Score 372.5; DB Pred. No. 4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 378.5; DB 4
Pred. No. 8.9e-34;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                            ACF9B1253ACA1E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                              DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                                                                                                                                                                                                                                                                                                                107;
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                                                                                                                                                                                                                                                                      Gaps
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RESULT
Q9UL79
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Best Local S
Matches 68
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                 Q9UL79;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
NON TEP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF035033; AAD56269.1; HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                    MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
Medis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            Q9UL79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                        EMBL;
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
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                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 1 1
                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                       +
                                                                 InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v
                                                                                             HSSP; P01607;
              NON_TER
                                                                                                                                                                              'Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIOMTOSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASYGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                      SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                          DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESGSGSGTDETLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. Immunopathol. 87:184-192(1998)
                                                                                                           AF035035; AAD56271.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
107
108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                108
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11501 MW;
                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
11787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 362; DB 4;
Pred. No. 5.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               070549FDE0754748 CRC64;
 DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                        MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                 and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
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Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9OYFO PRELIMINARY; PRT; 298 AA.
09OYFO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRATN=BALB/C; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00400; IGv; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB036341; BAA88633.1; HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                      Q9UL78;
                                                                   Q9UL78
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          method.
                                                                                                                                                                                         169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLAD
                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS
                                                                                                                                                                                                         77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCFV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFSGSGSTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107
                                                                                                                                       GVPSRFSGSGSTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N., Demura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEC-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                    298 AA; 31867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                 Conservative
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.0%; Score 346.5; DB 4; 64.5%; Pred No. 2.7e-30; Mismatches 25;
                                                                                                                                                                                                                                                            50.2%; Score 341.5; 57.7%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukuda H.;
                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    E0F96B8A17004317 CRC64;
                                                                       PRT;
                                                                                                                                                                                                                                                  Mismatches
                                                                       109
                                                                                                                                                                                                                                                               3e-29;
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                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
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                                                                                                                                                                                                                                                                             Length
     REGION (FRAGMENT)
                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:5947).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω99М37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF035036; AAD56272.1; -.
HSSP; P01789; 1MCP.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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Mammalia; Eutheria; Primates;
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                                                                                                                                   YQHKPGKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL- 114
                                                                                                                                                                                         MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW 59
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SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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Pred. No. 9.6e-27;
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                   01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                         Q9UL86;
                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
HSSP; P01789; 1MCP
           EMBL; AF035028; AAD56264.1;
                                     -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                        Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                          fetus."
                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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MEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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InterPro; IPR003596; Ig_v.
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                              DOMAIN.
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QOUL83;
QOI-MAY-2000 (TrEMBLrel. 13, Created)
QOI-MAY-2000 (TrEMBLrel. 13, Last sequence update)
QOI-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                   RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                                                                         RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK
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IMILARITY: TO IMMUNOGLOBULIN AND MAJOR H
                                                                                                                                                                                                                                                                                                                                          58.
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  (TrEMBLrel.
                                                PRELIMINARY;
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54.6%;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN
VARIABLE REGION (FRAGMENT).
Schistosoma Japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neo
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
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                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B.,
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B.,
"Construction and sequencing of the single-chain
"Construction and sequencing of the single-chain
human TNF-alpha specific monoclonal antibody.";
human TNF-alpha specific monoclonal antibody.";
                                                                                                                                                                                              Chen P.,
"Cloning
genes of
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J. Cel
                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN THE-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
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                                       SEQUENCE FROM N.A. Chen P., Deng J.B., Wang Z.L., Han H., Yao L.E Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 GSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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 AF262753;
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Deng J.B., Wang Z.L., Han H., Su C.Z.;

and sequencing of the light chain fragment
an anti-hrwr-a monoclonal antibody.";

Mol. Immunol. 12:21-26(1996).
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  AAG23804.1;
                            TO IMMUNOGLOBULIN
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Pred. No. 4e-25;
4; Mismatches
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                              AND
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                              MAJOR
                                                     Yao L.B.,
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HISTOCOMPATIBILITY
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Best Local Similarity 56.4
Matches 57; Conservative
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Best Local
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InterPro; IPR003006; Ig_wHC.
InterPro; IPR003006; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
NON_TER 107 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A.CA;

Malkiel S., Liao L., Cunningham M.W., Diamond B.;

"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";

submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-i-SMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9JL78 PRELIMINARY; PRT; 101 AA.
O9JL78;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF206028; AAF69326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 107 AA; 11784 MW;
                                                                                                                                                                                 88 GRDYSFNISNLEPEDIATYYCLQYDNL--WTFGGGTKLEIK 126
                                                                                                                                               61 GTSYSLTIGTMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK 101
                                                                                                                                                                                                                                                                                                 61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL 107
                                                                                                                                                                                                                                                                 1 TTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSPKLLIYRTSNLASGVPTRFSGSGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 101
101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;
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                            2002, 12:31:42
                                                                                                                                                                                                                                                                                                                                                                                                                      43.0%; Score 292.5; DB 1
56.4%; Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.5%; Score 295.5; DB 11; Lengtl 51.4%; Pred. No. 9.7e-25; tive 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 101;
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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein -
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                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                         Query
Match
100.0
100.0
86.5
84.9
84.3
83.8
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           : /SIDSB/gcgdata/geneseq/yeneseqp/AA1980.DAT: *
:/SIDSB/gcgdata/geneseq/yeneseqp/AA1981.DAT: *
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AAR81327
AAW22410
AAR81330
AAW04379
AAR11384
AAR76664
AAR71879
AAW21845
AAW21845
AAW63828
AAR81333
AAW22428
                                          Murine ONS-21 anti
V heavy chain of r
Heavy chain variab
Human Mab #117-10C
                                                                                                                                                                                                                                                           Description
  Human VLA-4 reshap
Humanised alpha-4
                                                                                                                             Chimaeric human/mu
Variable gamma hea
                                                                                                                                                                        Alpha-4 integrin m Mouse anti-VLA-4 a
                                                                                                                                                                                                                   Mouse VLA-4 antibo
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Mab #117-1 ormant CDM	AAW63820 AAW63830	19 19	119 248	67.2 67.2	501 501
e ch	AAR15443	12	240		501.5
	AAR15437	12	116		501.5
Chimaeric human/mu	AAW04396	17	136		502
$\overline{}$	AAR76681	16	136		502
VEGF antagonist an	AAB82701	22	136		503
Murine anti-botuli	AAY30123	20	254		504
Murine anti-botuli	AAY30121	20	254	•	504
Murine anti-botuli	AAY30119	20	254	•	504
Murine anti-botuli	AAY30117	20	254	67.6	504
Anti-HMFG MAD CTMO	AAW29750	18	139	•	505.5
MAD CT-M-01 heavy	AAY56873	21	138	•	505.5
	AAR39566	14	120	•	508
Heavy chain variab	AAR15439	12	126		509.5
	AAB73462	22	120	•	511
Anti VLA-4 antibod	AAY01033	20	120	•	511
ody HE	AAY23984	20	120		511
4 Ab HE	AAR58749	15	120	•	511
HP1/2 Vh. Homo sa	AAR39817	14	120	68.5	511
Heavy chain variab	AAW96744	20	121		513
Heavy chain variab	AAW96741	20	121		ر.
Anti-EGFR antibody	AAR79889	16	120		516.5
VLA4	AAR59942	15	143		517
chai	AAR60527	15	113		8
	AAW44121	19	120		₩
Heavy chain variab	AAR30767	14	120		₩.
chain	AAY53590	21	122	0	
ß	AAW37738	19	437		U
Humanised alpha-4	AAW22413	18	123	2	537
A heavy chain vari	AAB07969	21	135		
zed VLA-4 a	AAR81323	16	123	2	
HNK-20 variable he	ū	17	137	76.5	0
D)	AAB07967	21	135	7.	76.

## ALIGNMENTS

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

Mouse VLA-4 antibody 21.6 light heavy variable region.

23-MAR-1996 (first entry)

AAR81327;

AAR81327 standard; Protein;

140

antibody engineering.

RESULT AAR81327

ب

Key Peptide Region Mus musculus W09519790-A1. Region Region Region Region Region Region /note= " 86..117 /note= "c 132..140 /note= 69..85 /note= /note= 20..49 /note= "framework region 3"
118..131 50..54 Location/Qualifiers note= "signal peptide" "framework region 4" "complementarity determining region "framework region 2" "complementarity determining region "framework region 1" "complementarity determining region

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RESULT
AAW22410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are Constant regions. In the humanizing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27. Constant regions. In the humanized heavy chain, anino acids H27. Constant regions. In the humanized heavy chain, anino acids H27. Constant regions. In the humanized heavy chain, anino acids H27. Constant regions. In the humanized heavy chain, anino acids H27. Constant regions. In the humanized nework are replaced by the amino acid present in the equivalent position of the mouse CC 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are considered into COS cells. The humanized antibodies can be used CC to inhibit adhesion of a leukocyte to an endothelial cell and CC to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, comeningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibodies antibo
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Best Local
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Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                               Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                             08-DEC-1997 (first entry)
                                                                                                                                                                                                                                     AAW22410
                                                                                                                                                                                                                                                                              AAW22410 standard; Protein; 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                            121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKCSWYMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eqglewigridpangytkydpkfqgkatitadtssntaylqlssltsedtavyfcaregy 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1995-269276/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 746; DB 16;
Pred. No. 5.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermaitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially
                                                                                                                                     This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28 CL framework to produce a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS,
                         equivalent
                                                                                                                                                                                                                                               Claim 18; Page 69-70; 107pp; English.
                                                                                                                                                                                                                                                                                    Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                           asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                         Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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acute leukocyte mediated lung injury; therapy.
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                       to that
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69..85
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55,.68
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50..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Leader
                   of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                        Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "framework region
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                                                                                                                                                                                                                                                                          dementia,
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                                                                                                                                                                                                                                                                                      for treatment
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Query Match 100. Best Local Similarity 100. Matches 140; Conservative

100.0%; S 100.0%; P 1tive 0;

Score 746; DB 18; Pred. No. 5.9e-60; Mismatches 0;

Length 140; Indels

0;

Gaps

Sequence

140

AA;

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RESULT
AAR81330
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                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR81330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR81330 standard;
                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                     antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                    Region
                                                                                                                                                                                     Region
                                                                                                                                                                                                                      Region
                                                                          25-JAN-1995;
                                                                                          27-JUL-1995.
                                                                                                           WO9519790-A1
        WPI; 1995-269276/35
                        Bendig MM, Jones TS,
                                        (ATHE-) ATHENA NEUROSCIENCES INC.
                                                         25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                          95WO-US01219
                                                         94US-0186269
                                                                                                                                                                                               /note= "mouse heavy chain variable framewor)
    region 3"
                                                                                                                                                                                                                                                       50..66
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                     113..123
                                                                                                                                                            /note= "mouse heavy determining
                                                                                                                                                                                                                       67..98
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                                                                                                                                                                                                                                                                                                                    /label= CDR1
                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                            /label= FR4
                                                                                                                                                                                                               /label= FR3
                                                                                                                                                                                                                                                /label= CDR2
                                                                                                                                                                                                                                                                                 /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 123
                                                                                                                          "mouse heavy light chain variable framework region 4" \,
                                                                                                                                                                                                                                                                                                           "mouse heavy
                       Leger OJ,
                                                                                                                                                                                                                                        "mouse heavy
                                                                                                                                                                                                                                                                "mouse heavy chain variable framework region 2"
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region 1"
                                                                                                                                                                              CDR3
                                                                                                                                                                                                                               determining
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                                                                                                                                                                                             region
                         Saldanha
                                                                                                                                                                                                                                chain variable complementarity region 2"
                                                                                                                                                             chain variable complementarity region 3"
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                                                                                                                                                                                                                                                                                                           complementarity
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Db Db

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New humanised antibodies against VLA-4 - used for inhibiting felukocyte adhesion to endothelial cells, partic. for treating pr leukocyte adhesion to endothelial cells, partic. for treating pr leukocyte adhesion to endothelial cells, partic. for treating pr leukocyte adhesion to endothelial cells, partic. for treating pr leukocyte adhesion of sequence levels, cloned cDNA cDR sequences of constant framework regions of the REI antibody for the light chain and constant framework regions of the REI antibody for the light chain and constant framework regions of the REI antibody for the light chain and constant framework regions of the REI antibody for the light chain and constant fregions. In the humanized light chain, human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the humanized light chain, amino acids L45, L49, constant regions. In the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used for detecting VLA-4, for affinity purification or for generating cused for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.

NX Squence 123 AA;
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Query Match
Best Local
                                                                                                                                                                                                                                                  Matches
AAW04379 standard; Protein; 136 AA
                                                                       121 v 121
                                                                                                    140 V 140
                                                                                                                                                                                                       20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                61
                                                                                                                                                             80
                          4
                                                                                                                              evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 60
                                                                                                                                                            DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                  121;
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                86.5%; Score 645; DB 16; 100.0%; Pred. No. 6.5e-51;
                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                     0;
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AAW04379
                                                                                                                                                                                                                                                   RESULT
                                                                                                                                      Heavy; variable region; murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour;
                                                                                                                                                                                              04-DEC-1996
                                                                                                                                                                                                                AAW04379;
           Region
                                               Region
                                                                Peptide
                                                                                                             Synthetic
                                                                                                                               reshaped.
                                                                                                                                                                             Chimaeric human/murine MAb ONS-M21 variable heavy region
                            Region
                                                                                 Peptide
                                                                                                                                                                                             (first entry)
118..125
/label= C
                            /label= CDR_1
69..85
                                                /label= mat_peptide
50..54
                                                                /label= sig_peptide
20..136
                                                                                            Location/Qualifiers
                    /label= CDR_2
   CDR_3
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RESULT
AAR11384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the variable heavy region of the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols stranded Fv region. The reshaped Fv region has an agent for the diagnosis and treatment of cerebral tumours, e.g. myelphastoma.
      Peptide
                                          Mus musculus
                                                                           MAD T84.66; gamma heavy chain; carcinoembryonic antigen; CEA,
                                                                                                      Variable gamma heavy chain of T84.66 monoclonal antibody.
                                                                                                                                  08-MAY-1991 (first entry)
                                                                                                                                                                                    AAR11384 standard; Protein; 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                   human adenocarcinoma; mouse-human chimaeric antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. myeloblastoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-358509/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT38600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1994;
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                                                                                                                                                                                                                                                               121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                Match 84.9%; Score 633; DB 17; Length 136; Local Similarity 89.3%; Pred. No. 8.8e-50;
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                                                                                                                                                                                                                                                                                                                                                                            1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                  136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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     Location/Qualifiers 20..38
                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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AAR76664
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Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis.
                                         Murine ONS-21 antibody variable heavy chain.
                                                                   16-JAN-1996 (first entry)
                                                                                                    AAR76664;
                                                                                                                           AAR76664 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnose human colon adenocarcinomas. See also AAQ10834-Q10848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The heavy chain variable region of murine MAb 84.66 was cloned and sequenced. It was used to produce mouse V-human C antibodies with high affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel anti-CEA antibody - comparable to ATCC Accession No. BH 8747, produced by recombinant DNA, used in diagnosis of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shively JE, Riggs AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ11098.
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                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                         61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                             y--vsdyamaywgqgtsvtv 138
                                                                                                                                                                                                                                               eqglewigridpangnskyvpkfqgkatitadtssntaylqltsltsedtavyycapfgy 120
                                                                                                                                                                                                                                                                                                                                                               123;
                                                                                                                                                                                                                                                                                                                                                                                                                             140 AA;
                                                                                                                                                                                                                                                                                                                                                            Conservative
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39..49
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/note= "sequenced as peptide fragment"
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                                                                                                                                                                                                                                                                                                                                                                      84.3%;
87.9%;
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                                                                                                                                                                                                                                                                                                                                                         Score 629; DB 12; Length 140; Pred. No. 2.1e-49; 6; Mismatches 9; Indels
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RESULT
AAR41679
ID AAR4
XX AAR4
AC AAR4
XY 24-P
TY 24-P
XX V he
XX V he
XX Infe
KW Anti
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                    AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the murine antibody ONS-21 variable heavy chain. The plasmid was used in the construction of an expression vector, conty. CDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohtomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 59; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-1994;
                                                             V heavy chain of recombinant anti-feline calcivirus antibody.
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHUS
                                                                                                      AAR41679;
                               infection;
                                         Antibody; feline calcivirus; FCV; neutralise;
                                                                                  24-MAR-1994
                                                                                                                          AAR41679 standard; Protein;
                                                                                                                                                                             120
                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1995-200347/26
                                                                                                                                                                                                                   mkcswvmfflmavvtgvnsevqlqqsraelvkpgasvklsctasgfnikdtyihwakqrp 60
                                                                                                                                                                             yvn----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                                                                                      124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ94485
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato K,
                                                                                                                                                                                                                                                                                                                                                         136
                              diagnosis;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                           -qdywgqgtsvtv 134
                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
20..136
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 1..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchiya M;
                                                                                 entry)
                                                                                                                                                                                                                                                                                                               83.8%;
                               treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                           136
                                                                                                                                                                                                                                                                                                     Score 625; DB 16;
Pred. No. 4.6e-49;
2; Mismatches 8;
                                                                                                                           ₿
                              prophylaxis.
                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                       Indels
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RESULT
AAW21845
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                        The gene fragment encoding the V heavy chain region is used to produce a genetically engineered antibody capable of reacting specifically with feline calcivirus (FCV). The antibody can be to treat, prevent and diagnose FCV infection. It has a broad vineutralising spectrum and can be used to neutralise viruses which have acquired immunity to other neutralising antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                            Complementarity determining region; CDR; heavy chain; twariable region; murine; mouse; human; interleukin 5; receptor; alpha chain; monoclonal antibody; hybridoma; assay; diagnosis; allergic respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1-2; Figure 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-feline calcivirus recombinant antibody - used to treat, prevent and diagnosis infection and is safe but effective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ48001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-296521/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tokiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kimachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP561194-A.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAGA ) CHEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1993;
                   chronic bronchitis
                                                                                 Heavy
                                                                                                       19-DEC-1997
                                                                                                                            AAW21845;
                                                                                                                                                AAW21845
                                                                                                                                                                                                     121
                                                                                                                                                                                                                121 YGNYGYYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                              eqglewigridpangntkydprfqgkatitadtsfntaylqvnsltsedtavyy casggn\\
                                                                                                                                                                                                                                                        EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                  116;
                                                                                 chain variable
                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                        136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maeda H,
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   -laywgqgtlvtv
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERO THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92JP-0079189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93EP-0103066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Complementary
69..86
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118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                             79.8%;
82.9%;
                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mikami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementary Determining Region
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                                                                                                                                                                                                                                                                                                                                 Score 595; DB 14;
Pred. No. 2.3e-46;
8; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RES
                                                                                  KM1486 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishiyama
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                                                                                                                                                                                                                                                                                                                                                       Length 136;
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                              treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
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XXX
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                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                   murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAb) KM1486. KM1486 is produced by the hybridoma FERM BP-5651, which was prepared by immunising Balb/c mice with hull-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma 93-Ul cells and screening the resultant hybridomas. The MAb can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
 28-SEP-1998
                            AAW63828;
                                                  AAW63828 standard; Protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody against alpha-chain of human interleukin 5 receptor useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Pages 124-125; 238pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                               to treat such diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1995;
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                                                                                                                  117
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                                                                                                                                        121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                    61
                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                             1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is the heavy chain variable region of the
                                                                                                                                                                              EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                mkcswvifflmavvtgvnsevqlqqsgaelvkpgasvnlsctasgfnikdtymhwvkqrp 60
                                                                                                                                                               eqglewigridpangntksdpkfqakatiaadtssntaylqlssltsedtavyyct----
                                                                                                              -gglrlrffdywgqgttltv 135
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
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                                                                                                                                                                                                                                                                                                                                       137
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Takatsu )
(first entry)
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                       ĀĀ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-JP02588
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69..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= mat_peptide
50..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= sig_peptide
                                                                                                                                                                                                                                                                                 79.6%;
82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity_determining_region_3
                                                                                                                                                                                                                                                                                  Score 593.5; DB 1
Pred. No. 3.2e-46;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koike M;
                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                              Length 137;
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Db Qy

61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

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Query Match
Best Local Similarity
Matches 117; Conserv
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21-FEB-1997;
06-JUN-1997;
                                                                                                                                                                                                                                              gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease, leukopaenia, Behcet's disease, climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
                                                                                                                                                                                                                                                                                                                                                         discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
                                                                                                                                                                                             apitoxin-allergy and septic shock resulting from producti administration of excessive gamma interferon (IFN-gamma).
                                                                                                                                                                                                                  asthma, atopic dermatitis, allergic nastitis, pollinosis, apitoxin-allergy and septic shock resulting from production or
                                                                                                                                                                                                                                                                                                                                            syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
                                                                                                                                                                                                                                                                                                                                                                                                               Such antibodies can also be used to detect the II-18 receptor protein (labelled with an enzyme or a radioactive or fluorescent substance). The protein is used to treat e.g. graft rejection, pernicious anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human monoclonal antibody (Mab) #117-10C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New interleukin-18 receptor protein used to inhibit interleukin-18, to treat autoimmune disease and as immunosuppressant - and new monoclonal antibody and hybridoma used to detect interleukin -18
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain variable region which is used in a method involved in neutralising IL-18 or to treat autoimmune diseases or as an immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3.3a; Page 22; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-335317/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunikata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-18: IL-18; human; treatment; autoimmune disease; Mab; immunosuppressant; inhibitor; receptor protein; detection; heavy chain; monoclonal antibody; Mab; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Mab #117-10C heavy chain variable region protein fragment.
AAV44000
                                                                                                                                                                   138 AA;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0215490.
96JP-0356426.
97JP-0052526.
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                                                                                          79.2%;
83.0%;
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                                                                           4; Mismatches
                                                                                          Score 591; DB 19;
Pred. No. 5.5e-46;
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                                                                                                          Length 138;
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chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH (AAQ9889) and VL (AAQ9889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5 and 3 ends of the mouse cDNAs are modified using PCR primers (AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the
                                                                                                                          The sequence represents the human reshaped antibody 21.6 heavy
                                                                                                                                                  Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                      25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                               27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VLA-4 reshaped antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR81333 standard;
                                                                                                                                                                            inflammatory disease.
                                                                                                                                                                                      New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                           N-PSDB; AAQ99894.
                                                                                                                                                                                                                                       WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                              25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanized antibody; leukocyte adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR81333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                              94US-0186269
                                                                                                                                                                                                                                                                                                                                      95WO-US01219
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118..131
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86..11
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
132..1
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50..54
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20..49
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                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                           .142
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                             "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region
                                                                                                                                                                                                                                                              Leger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                               ο<u>υ</u>,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                               Saldanha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecule;
                                                                                                                                                                                                                                                                Ç.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLA-4;
                                                                                                                                                                                       for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic;
  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can
                                                                                                                                                                                                                                                                                                                                                                               asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                          Region
                                                                                                                                                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW22428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebral traumas, meningitis or encephalitis. The antibodic also be used for detecting VLA-4, for affinity purification
                                                              Region
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                                                                                                                                                                         Region
                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22428 standard; Protein; 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mdwtwrvfcllavapgahsqvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ygnygvyamdywgqgtlvtv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gqrlewmgridpangytkydpkfqgrvtitadtsastaymelsslrsedtavyycaregy
                                                                                                                                                                                                                                                                                                                                                           leukocyte mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
                                                                                                                                                                                                                                                                                                                                                                        dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                            synthetic
                                                                                                                                                                                                                                                                                                                                 Mus musculus;
                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                       sapiens;
                                                                                                                                      /note=
55..67
                                                                                                                                                                         /note=
50..55
                                                              /label= CDR2
/note= "21.6 complementarity determining
86..117
                                                                                                  /note= "21/28'CL 68..85
 /note= "21.6 complementarity determining
                          /note= "21/28'CL
118..131
                                                                                                                                                                                                                       /label= Mat_protein
/note= "VH version
                                                                                                                                                                                                                                                           /label= Leader
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                   /label=
                                                                                                                         /label=
                                                                                                                                                              /label= CDR1
                                                                                                                                                                                                  /label= FR1
                                                                                                                                                                                                                                                                                                                                                          psoriasis; myocardial ischaemia;
diated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%;
77.1%;
                                                                                                                                                 "21.6
                                                                                                                                                                                     "21/28'CL
                                                   FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 584; DB 16; Pred. No. 2.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
A
                                      framework region
                                                                                                                                                                                    framework region
                                                                                                            framework region
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                                                                                                                                                                                                                                                                                                                                                                                                                                           21.6 VL version Ha.
                                                                                                                                                                                                                         (Claim 25)"
                                                                                                                                                 determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 142;
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                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                          AAB07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This polypeptide, designated Ha, comprises the heavy chain variable CC region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also CA AW22413). It is composed of complementarity determining regions from CC the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal CC antibody 21.6 and a modified human 21/28/CL framework. It can be CC expressed in mammalian host cells following PCR amplification and CC mutagenesis of appropriate mouse and human DNA sequences. The CC mutagenesis of appropriate mouse and human DNA sequences. The CC mannised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used CC to produce a claimed humanised 21.6 VL (see AAW22412) can be used CC to produce a claimed humanised 21.6 vL vice AAW22412) can be used CC aritised 21.6 vL antibody that is useful in the CC mannised cure of a medicament for treating asthma, atherosclerosis, CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid CC aritists, transplant rejection, graft versus host disease, tumour CC metastasis, nephritis, atopic dermatitis, proriasis, myocardial CC ischaemia, and acute leukocyte mediated lung injury. The humanised CC antibody has a half-life in the human circulation essentially
     autoimmune
                                                                                                                                                                       AAB07967 standard; Protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Fig 11; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1996;
                     Antibody 1f1; B7 molecule; B7; humanised immunoglobulin;
                                                        Amino, acid sequence of heavy chain variable region of 1F1 antibody
                                                                                                  14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uses of humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                    121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                   ygnygvyamdywgggtlvtv 140
                                                                                                                                                                                                                                                                                                                                          gqrlewmgridpangytkydpkfqgrvtitadtsastaymelsslrsedtavyycaregy
                                                                                                                                                                                                                                                                                                                                                           EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis, AIDS,
   disease; infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "21/28'CL framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 584; DB 18; 77.1%; Pred. No. 2.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR4
disease; inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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egglewigwidpengntlydpkfqgkasitadtssntaylqlssltsedtavyycaregl 120

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                            molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematorys, diabetes mellitus, insultis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the heavy chain variable region of the murine antibody 1F1. The antibody has a binding specificity to B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aplastic anaemia; myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Fig 6A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1999;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2000; 2000WO-US03303
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                                                                                                                                                                                                                                                                                                                                                                           thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine antibody 1F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC.
61
                                                                                                                                                                                     Local Similarity
                                                                           1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GS,
EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                               \verb|mkcswvifflmavvtgvnsevhlqqsgaelvrpgalvklsckpsgfnikdyymhwvkqrp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-524532/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vasquez M,
, Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin having a binding specificity to B7-1 (derived PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                             135 AA;
                                                                                                                                                                                                                                                                                                                                            a and aplastic anaemia), inborn errors of metabolism, immunodeficiency diseases, and myeloid dysplasia syndrome.
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0339596
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69..85
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50..54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carreno
O'hara
                                                                                                                                                                                   77.3%;
80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region
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                                                                                                                                                         6;
                                                                                                                                                                                   Score 576.5; DB 2
Pred. No. 1.1e-44;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker AC,
Rup B, Veld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Veldman GM;
                                                                                                                                                                                                            DB 21;
                                                                                                                                                         14;
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                                                                                                                                                         Indels
                                                                                                                                                                                                            Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region 1"
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                                                                                                                                                         7;
                                                                                                                                                         Gaps
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121 YGNYGVYAMDYWGQGTSVTV 140

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                                                                                                                                                                                                                             CC AAR95946-R95948 represent sequences for variable regions of an antibody CC produced by the hybridoma cell line HNK-20. This sequence represents CC the sequence for the antibody HNK-20 variable heavy chain. HNK-20 is a CC murine hybridoma cell line, that produces IgA specific for the F CC quitranslated region, that produces IgA specific for the 5 CC untranslated region of the variable region, and for the intron CC containslated region of the variable region, and for the intron CC downstream of the rearranged J region (see AAT30459-T30545 for primer Sequences). The DNA encoding these sequences can be inserted into vectors CC sequences). The DNA encoding these sequences can be inserted into vectors CC containing heterologous (such as human) constant region genes, for the CC are useful in the treatment and diagnosis of infection by RSV, such as penumonia and bronchiolitis, in humans and animals. By using genomic DNA CC as a template, variable region genes can be isolated without producing CC fragments that have to be adapted for recombinant antibody expression. CC contain the target variable region is required. Chimeric antibodies conding the target variable region is required. Chimeric antibodies conding the target variable region is required. Chimeric antibodies conding the target variable region is required. Chimeric antibodies conding the target variable region is required. Chimeric antibodies conding the target variable region is required.
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                                                                                Matches 114;
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse; F glycoprotein; respiratory syncytial virus; RSV; constant region gene; chimeric antibody; isotype-switched antibody; therapy; infection; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Fig 5d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR95948 standard; Protein; 137
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory syncytial virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding variable region of antibody HNK-20 - for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-286826/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berdoz J, Kraehenbuhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ORAV-) ORAVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumonia; bronchiolitis; animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1997 (first entry)
                                                                                                                                                                                                                   host being treated, are less likely to cause adverse immune reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 f-----faywgqgtpvtv 133
                                                                                                    Local Similarity
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                                          --
AAT30458
                                                                                                                                                                               137 AA;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0348548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75pp; English
                                                                                                  76.5%;
81.4%;
                                                                                6
                                                                                                Score 570.5; DB 1
Pred. No. 3.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                Mismatches
                                                                                                                    DB 17;
                                                                                15;
                                                                                Indels
                                                                                                                  Length 137;
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                                                                              Gaps
                                                                                2;
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QΥ

20 EVOLOOSGAELVKPGASVKLSCTASGFNIKDTYIHCVKORPEQGLEWIGRIDPANGYTKY 79

Matches 100;

Conservative

11;

Local Similarity

72.9%; 82.6%;

Score 544; DB 16; Pred. No. 8.2e-42; 1; Mismatches 10;

Length 123; Indels

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AAR81323
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The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L48, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting inflammator. Afocaco couch as mendothelial cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81323 standard; Protein; 123
                                                                   for treating inflammatory diseases such as multiple sclerosis. can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 69; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1996
Sequence
                                anti-idiotype antibodies.
                                                  meningitis or encephalitis. The antibodies can also be used detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
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123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones TS,
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                      The present sequence represents the heavy chain variable region of the humanised murine antibody IFI. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized
                                                                                                                                                                                                             Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                    Example 10; Fig 7A; 162pp; English.
                                                                                                                                                                                               diseases, infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Co MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
  immunoglobulins, which comprise an antigen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-1999;
24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aucoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody 3D1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A heavy chain variable region of humanised 1F1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 v 121
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O'hara D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulitus, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thalassemia and aplastic anaemia), inborn errors of metabolism,
                                                                                      121 f-----faywgqgtlvtv 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
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US-08-8561-521-4
PCT-US95-01219-44
US-08-561-521-11
PCT-US95-15716-8
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US-08-952-8008-13
US-08-952-8008-2
PCT-US93-00034-2
PCT-US93-0024-2
US-08-603-22-8008-2
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US-08-452-164A-8
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63.5	63.7	63.7	63.7	63.7	63.7	63.7	64.7	64.8	64.8	65.5	66.3	66.8	67.1	67.3	67.6	67.6	67.6
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Sequence 4, Appli	Sequence 18, Appl	Sequence 15, Appl	Sequence 18, Appl	Sequence 86, Appl	Sequence 86, Appl	Sequence 86, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 19, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 38, Appl	Sequence 99, Appl	Sequence 13, Appl	Sequence 10, Appl	Sequence 7, Appli

## ALIGNMENTS

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RESULT 1
US-08-561-521-4
                                                                                                        ; MOLECULE TYPE: protein US-08-561-521-4
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                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                     FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/186,269A
APPLICATION NUMBER: US/08/186,269A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CITY: San Francisco
STATE: California
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100.0%; Score 746; DB 2; 100.0%; Pred. No. 1.5e-68; ...
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Query Match
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Matches 140; Conserv

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Best Local Similarity
                                                                                                                                                                                               Matches 140;
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLACES: 25-JAN-1994
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
NAME: Smith, William J.
15
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APPLICANT:
APPLICANT:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Humanized Antibodies AgriTITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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121 YGNYGVYAMDYWGQGTSVTV 140
                                                    61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                              1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                           1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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amino acid
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                                                                                                                                                                                         100.0%; Score 746; DB 5; Length 140; ilarity 100.0%; Pred. No. 1.5e-68; Conservative 0; Mismatches 0; Indels
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Saldanha, Jose
Jones, S. Tarran
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Leger, Olivier J.
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Sequence 9, Application PC/TUS9501219 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US/08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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                                                                                                            121 V 121
                                                                                                                                             140 V 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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100.0%; Pred. No. 2.2e-58;
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                                                                                                                                  Sequence 29, Application US/08646265A Patent No. 6214973
GENERAL INFORMATION:
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Best Local
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                APPLICANT: OHTOMO, TOShihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
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                   CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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 ADDRESSEE:
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21; Conservative
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amino acid
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Leger, Olivier J.
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Foley & Lardner
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100.0%; Pred. No. 2.2e-58;
tive 0; Mismatches 0;
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APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
                                                                                                GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOHYA, Yukinobu
APPLICANT: TOHYA, Yukinobu
APPLICANT: MIKAMI, Takeshi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELEFAX: (202)672-5399
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MEDIUM TYPE: Floppy disk
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                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, C
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CITY: W
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CITY:
STATE:
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Washington D.C.
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                               E: WEGNER, CANTOR, MUELLER & PLAYER 1233 20th Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 amino acids
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89.3%;
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COUNTRY:

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US-08-836-561-31
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                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08836561 Patent No. 6018032
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Best Local (
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEX: 440706 WEGBR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Aga
TITLE OF INVENTION: Receptor Alp
           ZIR: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     121 AW-----LAYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YGNYGYYAMDYWGQGTSVTV 140
 COMPUTER:
                                                                            STATE:
                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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REGISTRATION NUMBER: 2
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                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20036-8218
                                                                                                      E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                            USA
                                                                                                                                                                                                                                             NAKAMURA, Kazuyasu
IIDA, Akihiro
                                                                                                                                                                                                                                                                            FURUYA, Akiko
                                                                                                                                                                                                                                                                                           KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
IBM Compatible
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82.9%; Pred. No. 3e-53;
ative 8; Mismatches
                                                                                                                                                             Antibody Against Human Interleukin-5
Receptor Alpha Chain
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US-08-561-521-17; Sequence 17, A; Patent No. 584;
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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TELECOMMUNICATION INFORMATION: 212-790-9090
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ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YGNYGVYAMDYWGQGTSVTV 140
                   CLASSIFICATION:
                                  APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                                      SOFTWARE:
                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                  COUNTRY:
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TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
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STRANDEDNESS: sir
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SOFTWARE: FastSEQ Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 09-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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5840299
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                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                 Leger, Olivier J.
Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                    Bendig, Mary M.
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09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%; Score 593.5; DB 3; 82.9%; Pred. No. 4.2e-53;
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ATTORNEY/AGENT INFORMATION:

William L

APPLICATION NUMBER: US/08/186,269A FILING DATE: 25-JAN-1994

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
; GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                  PRIOR APPLICATION NUMBER: US 08/186,269
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 31,223
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                 REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YGNYGYYAMDYWGQGTLVTV 140
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                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120
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                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                    415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-17
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-561-521-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 44, Application US/08561521
Patent No. 5840299
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Best Local Similarity
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                                                                                                                                  TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
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LENGTH: 142 amino acids
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                         NAME: Smith, William L. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                      STRANDEDNESS:
                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP
                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One Market Plaza,
                                                                                        125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                    415-543-5043
                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Crew e Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                         415-543-9600
                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.3%;
77.1%;
                                                                                                                                                                                                                             30,223
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                                                                                                                                                                                                                 15270-14
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                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/186,269

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 110;
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY--GNYGVYAMDYWGQGTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 VTV 140
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                                                                    20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQCLEWIGRIDPANGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                San Francisco
                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                      125 amino acids
                                                                                                                             Conservative
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Jones, S. Tarran
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                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                        single
                                                                                                                                          75.3%;
89.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US95/01219
                                                                                                                           2; Mismatches
                                                                                                                     Score 562; DB 5; Length 125; Pred. No. 5.9e-50; 2; Mismatches 9; Indels
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PCT-US95-15716-8
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                                                         RESULT
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Sequence 8, Application PC/TUS9515716 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
DETERPEROFACTORY NUMBER: 06132/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                             117 YGT--SYWFPYWGQGTLVTV 134
                                                                                                                                                 121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                   60 EQGLEWIGWIDPENGNTYYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 116
                                                                                                                                                                                                     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                         Match 74.3%; Local Similarity 80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VTV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                           1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                     Score 554; DB 4; Length 136;
Pred. No. 4.3e-49;
6; Mismatches 15; Indels
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APPLICANT:

Berdoz, Jose

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                                                                                                                                                                                                                    GENERAL INFORMATION:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEBAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                        APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                117 YGT--SYWFPYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                     121 YGNYGYYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Pred. No. 4.3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 123 amino acids
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MEDIUM TYPE: Floppy disk
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                              TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                SOFTWARE:
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ARE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA:
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APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
Search completed: May 7, 2002, 12:23:04 Job time: 175 sec
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and is derived by analysis of the total score distribution.
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Ig heavy chain v r
Ig heavy chain pre
Ig heavy chain pre
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Ig heavy chain V r
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Ig heavy chain V r
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Ig heavy chain V r
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Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involv A; Reference number: S04573; MUID:87133856
A;Accession: S04573; MUID:87133856
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <MAT>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

Qy DЬ 20

YAMDYWGQGTSVTV 140

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116 127 61 67

YGMDYWGQGTSVTV 129

S04576

Qy 7 MFFLMAVV7 :         Db 1 IFFLMAVV7	Query Match Best Local Similarity Matches 118; Conser	submitted to the EMBL Data Libra A; Reference number: S29593 A; Accession: S29594 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-178 <sey> A; Cross-references: EMBL: X57857; C; Keywords: immunoglobulin</sey>	hain Mus -Jan n: Sí		440 59 439 58 438 58	440 59 440 59		447	451.5 451	452 60		454	30 454.5 60.	
rgvnsevolo	vat	Data 29593 29583 Y> MBL: X5	C 01		. 0		0 - 1	. ס		. 6	7.9	.9	9 .	
QSGA       QSGA	80.9%; 88.1%; ive	Library, 7857; NI	e_re		222	NN	22			N	N N	2	2	
MFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTVIHCVKQRPEQGLEW :	Score 603.5; DB 2; Pred. No. 1.5e-45; 6; Mismatches 5;	ry, February 1991 NID:g52590; PIDN:CAA40992.	) - mouse (fragment) Lus (house mouse) #sequence_revision 06-Jan-1995 #tex	ALIGNMENTS	\$40295 \$20646 C37262	S20643 S38950	PH1488 S41394	PH1489	PH1494	PH1493	S21810 PH1484	\$25174	PC1155	
YIHCVK	Length Indels	)992.1;	#text_change		61 61 61	Ig PI	Ig 1 g	Iq Iq	bī fī	Ιġ	Iq Iq	ξīg	Ig	
VKQRPEQGLES              VKQRPKQGLES	178;	PID:g52591			gamma- heavy heavy	heavy gamma	heavý heavy	heavy heavy	heavy	heavý	heavy	heavy	heavy	
TEM 60      EM 66	Gaps	52591	05-Nov-1999		-2a chain chain V chain V	chain V chain -		chain V	chain V	chain	chain V r		chain pr	
	2;				4 H D	9 K	нн	нн	н -	н	н н	r	ro o	

F;34-117/Domain: immunoglobulin homology <IMM>

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PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1403
C;Accession: M: Minagon T · Haniwara. S.: Kimoto, H.; Shigemoto, K.; Tanig
A;Residues: 1%123 <SHI>
                                                                                                                        R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
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A)Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: himmunoglobulin homology <IMM>
                                                                                             ia virus.
                                                                                                                   A; Title:
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A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000 C;Accession: S52445 R;Berdoz, J.; Kraehenbuhl, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-137 <BER>
A; Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C; Genetics:
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A; Accession: S52445
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Best Local
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                                                                                                 Heavy chain variable (VH) region diversity generated by VH gene replacement in
                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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81.4%;
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82.9%;
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Pred. No. 8.4e-43;
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Ig heavy chain V region (E8) - mouse (fragment) c;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S17586
                                                                                                                                                          RESULT
S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D. J. Mol. Biol. 221, 455-462, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-43 < ROC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
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C:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-118/Domain: immunoglobulin homology <IMM>
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A; Residues: 7-120 < ROC1>
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                                                                                                                                                                                                                                                                                                                                                                               80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.3%;
89.3%;
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94.9%;
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Pred. No. 4e-40;
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bred. No. 1.4e-42;
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A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:x60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of mur
A;Reference number: S06813; MUID:90064531
A;Accession: S06823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #C;Accession: S03482; S07453
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A; Residues: 1-122 <MIL>
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Local Similarity 85.2%;
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                                                                                                                                                   TV 120
                                                                                                                                                                                                                                                  YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                               EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104;
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Pred. No. 9.6e-39;
                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4e-38
                                                                                                                                                                                                                                                                                                                                                                             Score 521.5; DB 2;
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                  26-Feb-1998 #text_change
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R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT A;Reference number: 807453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Moncharmont, B.
submitted to the EMBL Data Library, Se
A:Description: Cloning and sequencing
A:Reference number: S24287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma chain V region (JS34/32) - mouse C;Species: Mus musculius (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20:C;Accession: S24289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 10-115 < ROC1>
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                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963 C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                         F;14-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                               C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-116 < MON>
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Best Local Similarity
                                                                                                                          y Match 67.0%;
Local Similarity 81.0%;
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                                                  21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this sequence was determined from the differentiated gene Serra, J. Mazie, J.C., Moinier, D.; Leclercq, L.; Somme,
1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVOLQOSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
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                                                                                                         9;
                                                                                                                               Score 500; DB 2; Length 116; Pred. No. 9.5e-37;
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Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident:
A;Reference number: A56446; MUID:95229583
                                                                                                                                          A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-268 <TAN>
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A;Reference number: S07453; MUID:83058021
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 10-120 <ROC1>
A; Cross-references: EMBL: x07144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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A:Accession: S03484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. EMBO J. 2, 867-872, 1983
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                                                       Local Similarity
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                                   98;
                               Conservative
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                                                    66.3%;
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                               8; Mismatches
                                                       Pred. No. 6.8e-36;
                                                                     Score 494.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 498; DB 2;
Pred. No. 1.5e-36;
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                                                                     DB 2;
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                            Indels
                                                                     Length 268;
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A; Experimental source: strain Balb/c C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C; Keywords: immunoglobulin F;1-120/Domain: V region #status predicted < VRG>
                                                                                                                 F:121-221/Domain: C region #status predicted <C: F:139-203/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                 A; Cross-references: EMBL: Z37502; NID: g541778; PIDN: CAA85732.1; PID: g541779
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-221 <KIP>
                                                                                                                                                                                                                                                                                                                               A; Description: Cloning and A; Reference number: $49220 A; Accession: $49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar_1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Experimental source: B cell, strain [NZB x NZW]F1 C:Superfamily: immunoglobulin V region; immunoglobuc: Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S49220
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J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;15-98/Domain: immunoglobulin homology <IMM>
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A;Accession: PH1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
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Best Local :
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                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 YDPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCA-SYYLTRY----ENYWGQGTTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 YDDKFQGKATITADTSSNTAYLQLSSLTSEDTAYYFCAREGYYGNYGYYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
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       96;
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                             Similarity
       Conservative
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                                                                                                                                         region #status predicted <CRG>
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                          66.0%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                   Library, September 1994 expression of a recombinant mouse Fab-fragment recognizing
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                        Score 492; DB 2;
Pred. No. 9.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 493.5; DB 2
Pred. No. 3.3e-36;
    Mismatches
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                                             Length 221;
  Indels
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20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

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A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995 C;Accession: A47271  
R;Lesley, S.A.; Patten, P.A.; Schultz, P.G. Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993  
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic acti A;Reference number: A47271; MUID:93165660  
A;Accession: A47271
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                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Glusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
A;Reference number: PH1482; MUID:93171820
A;Accession: PH1482
A;Status: translation not shown
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-140 <GIU>
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C; Species: synthetic
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                                                                                                                                                      A; Experimental source: hybridoma cell
A; Experimental source: hybridoma cell
C; Genetics:
A; Introns: 16/1
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < TMM>
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                                  Query Match
Best Local Similarity
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63.1%;
Score 471; DB 2; pred. No. 3.8e-34;
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                                          Length 140;
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                          YG--GSYYFDYWGQGTTLTV 138
              YGNYGVYAMDYWGQGTSVTV 140
                                                                                    91; Conservative
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                                                                                     Mismatches
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Search completed: May 7, 2002, 12:23:47 Job time: 198 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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pri; 139 AA.  beguence update) nnotation update) nnotation update) nnotation update) nnotation update) /186-2 precUrsOr.  Craniata; Vertebrat; Sciurognathi; Murid; Reth M., Imanishi-Ka contribution to the evident in a gamma 2 MU CHAIN MRNA WAS CLO HAPTEN (4-HYDROXY-3	HV1H_HUMAN HV41_MOUSE HV05_CARAU HV36_MOUSE HV24_MOUSE HV3C_HUMAN HV3T_HUMAN HV3T_HUMAN HV3T_HUMAN HV43_MOUSE HV21_HUMAN HV4A_HUMAN HV4B_HUMAN HV4B_HUMAN HV4B_HUMAN HV4B_HUMAN HV1F_HUMAN
ae; Euteleostomi; ae; Murinae; Mus. ri T., Rajewsky K., Npb family of a variable region."; NED FROM A HYBRIDOMA NITROPHENYL)ACETYL	P80421 homo sapien P01811 mus musculu P19181 carassius a P01806 mus musculu P01793 mus musculu P01764 homo sapien P01781 homo sapien P01781 homo sapien P01781 homo sapien P01762 homo sapien P016331 homo sapien P01762 homo sapien P01762 homo sapien

Query Match Best Local Similarity

62.3%; 65.0%;

Score 464.5; DB 1; Pred. No. 8.1e-38;

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                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1. SMART; SMO0406; IGv; 1. SMART; SMO0406; IGv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal. SIGNAL 1 19
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InterPro; IPR003596; Ig_v.
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Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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    YG--GSYDEDYWGQGTPLTV 138
                         YGNYGYYAMDYWGQGTSVTV 140
                                              GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120
                                                                                        MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
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15514 MW;
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Pred. No. 2.7e-37
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         (NPB ANTIBODIES).
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_MOUSE MULTIPOUSE STANDARD; PRT; 137 AA PO1755; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1G HEAVY CHAIN V REGION S43 PRECURSOR.
                                                              antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                            MEDLINE=81234548;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 36-65.
                                                                                                             "Heavy chain variable region
                                                                                                                                                              Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
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"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Eur. J. Immunol. 12:1023-1032(1982).

-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                           '!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
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MEDLINE=83131846; PubMed=6186498;
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MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
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PIR; A02033; HVMST7.

InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                  fucker P.W.;
                                                                                                                                        MEDLINE=84248078; PubMed=6429663;
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                       fllegitimate recombination generates a
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                                                                                                                                                                                                                                                                                                                                                   YGNYGVYAMDYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                 GRGLEWIGRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-R 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
                                                                                                                                                                                                                                                                                                                                      LGRY----FDYWGQGTTLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                        EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                MGWSCIMLFLAATATGVHSQVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00047; ig; 1; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J00539; AAA38172.1; -.
                                                                                Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                Sci. U.S
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                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
                                                                                                                              Richards
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                                                                                                                                                                                                                                                                                                                                                             140
                                                                                 plasmacytoma.";
S.A. 81:4164-4168(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 422.5;
Pred. No. 8.
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JH2
BY S
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D SEGMENT.
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                                                                                                                     Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD5881BF44B8EC9 CRC64;
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                                                                                                                            Ε.,
                                                                                                                              Blattner
                                                                                                                                                                                                                                   update)
                                                                                                        class switch
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                                                                                                                             F.R.,
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                                                                                                                                                                                                    Euteleostomi;
                                                                                                                              Mushinski J.F.,
                                                                                                                                                                                        Murinae;
                                                                                                        from
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Query Match

Best Local Similarity

55.1**%**;

Score Pred.

411; No.

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DOMAIN
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P01753; P11271;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
                                            DOMAIN
DISULFID
NON_TER
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                                                                        DOMAIN
DOMAIN
                                                                                                                                                                              RELATED GENES THAT COULD PIR; B02034; HVMS61.
                                                                                                                                                                                                          "Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                          Pfam; PF00047; ig; 1. SMART; SM00406; IGV;
                                                                                                                                                                                                                                               Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                                        MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                     DOMAIN
                                                                                                               CHAIN
                                                                                                                        SIGNAL
                                                                                                                                                            InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                   -!- MISCELLANEOUS:
                                    SEQUENCE
                                                                                            DOMAIN
                                                                                                                                Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                               YYDWF-----VYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGWSYIILFLVATATDVHSQVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING FRAMEWORK 2. COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION TEPC 1017. FRAMEWORK 1.
                                                                                          IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                               FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
                                                                                                                                                                                                                                               Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                          ENCODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                      16191A088CB17F5A
                                                       SIMILARITY
                                                                                                                                                                                                   GENE
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                                                                                                                                                                                         REGIONS OF NPB ANTIBODIES
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DB 1;
.9e-33;
                                                                                                                                                                                                                    gamma
                                                                                                                                                                                                                              to the NPb family
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                                      CRC64;
                                                                                                                                                                                                                      2a variable
         Length 117;
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RESULT 8
HV06_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by two adjacent CH genes."; Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION BCL1 PRECURSOR.
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02042;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00494; AAA38130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82222262; PubMed=6806821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV15_MOUSE
                                                           119
                                                                                    121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                         61 AKSLEWIGVISTYNGNTSYNQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--Y 118
                                                                                                                                           61
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                               1 MKCSWVMEFILMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                                                                                                                                     EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                {\tt MGWSCIIFFLVATATGVHSQVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSH}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60
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136 AA;
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                                                                                                                                                                                                                                                                             136
15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                   53.1%; Score 396; DB 1; 55.7%; Pred. No. 2.9e-31;
                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION BCL1
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HV49_MOUSE
ID HV49_MOUSE
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NON_TER
SEQUENCE
This SWISS-PROT entry is copyright.
                                                    unrearranged VH gene segments."; Cell 40:271-281(1985).
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986
15-JUL-1999
                                                                                                "Developmentally controlled and tissue-specific expression
                                                                                                                                                       MEDLINE=85099340; PubMed=2578321;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, 01-JAN-1988 (Rel. 06, 15-JUL-1999 (Rel. 38,
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01-JAN-1988
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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
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       C02034;
                                   J00533; AAA38602.1;
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                                                                                                                                                                 non-profit institutions as long and this statement is not removed.
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   HVMS45
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No. 4.8e-31;
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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Query Match Best Local S Matches 75

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  RESULT 11
HV04_MOUSE
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Best Local :
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DOMAIN
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Iq v.
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                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
                                                                                                                                                       RELATED GENES THAT PIR; A02030; HVMS23.
                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 23 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                         HV04_MOUSE
                                                                                                                                                                                      Cell 24:625-637(1981)
                                                                                                                                                                                                "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                              Bothwell A.L.M., Paskind M.,
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                          DOMAIN
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                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                     Baltimore D.;
                                                                                                                                                                                                                                        MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                                                Reth M., Imanishi-Kari T., Rajewsky K.,
                                COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                   COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                       IG HEAVY CHAIN V REGION FRAMEWORK 1.
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                       BY SIMILARITY.
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   CRC64;
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HV13_MOUSE
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Best Local :
     HV13_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M13787; AAA38499.1; -. PIR; A02029; HVMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION VH558 Al/A4 PRECURSOR.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                             EWIGWIYPGDGSTKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
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No. 6.7e-30;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
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     PRT;
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Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANBOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                   SEQUENCE FROM N.A.

MEDLINE-81053741; PubMed-6253904;

Zakut R., Cohen J., Givol D.;

"Cloning and sequence of the cDNA corresponding region of immunoglobulin heavy chain MPCII.";

Nucleic Acids Res. 8:3591-3601(1980).
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
15-JUL-1999 (Rel. 38, Last annot
IG HEAVY CHAIN V REGION MPC 11.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION J558.
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(Rel. 01, Last sequence update)
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117
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InterPro; IPRO03006; Ig_wHC.
InterPro; IPRO03596; Ig_v.
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InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; ICv; 1.
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Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel bekker, New York (1978).
-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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MEDLINE=83065234; PubMed=6815656;

MENTAN MOLGAARD H.V., Houghton M., Derbyshire R.B., Viney J.,

Bell L.O., Gould H.J.;
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Pred. No. 1.1e-29;
                                                                            T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-I REGION ND PYRROLIDONE CARBOXYLIC ACID.
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        948F9F72A5366C20 CRC64;
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DYSYTLDVWGQGTTVTV 145
                                                WINPNSGGTNYAPREQGRVTMTRDASFSTAYMDLRSLRSDDSAVEYCAKSDPFWSDYYNF 128
                                                              RIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-----EGYYGN 123
                                                                                                                                                72;
                                                                                                FLVAAATRVHSQTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVG
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                                                                                                                                                               50.7%;
52.6%;
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                                                                                                                                                               Score 378.5; DB 1 Pred. No. 1.5e-29;
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Search completed: May 7, 2002, 12:32:34 Job time: 565 sec

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 AAR81321
AAW22412
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Humanized anti-VLA
Humanised alpha-4
Humanised alpha-4
Humanised alpha-4
Mouse anti-VLA-4 antibo
Human VLA-4 reshap
Alpha-4 integrin m
Human WCP-3 and mu
Human IP-10 and mu
Artificial synthet
ME1-14 light chain
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Human consensus	AAY82345	21	108	79.1	444.5
pUC-RVI-PMIa.	AAR29015	13	126	79.1	444.5
pUC-RVh-PMIa.	AAR29013	13	126	79.1	444.5
Interleukin-6 s	AAY55072	21	256	79.1	444.5
Single chain Fv	AAY55075	21	260	79.1	444.5
Consensus	AAB60400	22	107	79.1	444.5
Human var	AAB61585	22	107	79.1	
Human con	AAW70622	19	108	79.1	
Värläble Humanised Humanised Buman Vl	AAW86804 AAW70623 AAW87455	19 20	107 107 107	79.3 79.3	445.5
Anti-VEGF TF8-5G9 CD Protein en	AAW10233 AAW10703	19 18	110 234 237		446.5 446.5 446.5
variable Lig Variable Lig Humanised mu CDR-grafted	AAW35133 AAW86805 AAW70625 AAW10231	19 19	107 107 108	80.2 80.0 80.0	449.5 449.5 446.5
FWP51 fusion Human REI mon Human/murine	AAR26981 AAR65163 AAR47207	13 15	241 108 129		452 451.5 451.5
Humanized	AAR81322	16	107		453.5
Humanised	AAW22422	18	107		453.5
Murine OK	AAR13658	12	109		453
ScFv(FWP51).	AAR85495	16	240	81.0	455
Amino acid s	AAY21882	20	241	81.0	455
Anti-gp54 MA	AAW26800	19	245 -	81.0	55
Murine monoc Variable reg (FRP51)-ETA Anti-gp54 MJ	9855	17 13 19	108 128 637 109	82.7 81.9 81.9 81.1	465 460.5 460 456
CD4-sı	305	12	234		475.5
Light	897	16	107		471.5

# ALIGNMENTS

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Mus musculus. Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                               New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                        (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9519790-A1
                                                                                                                                                                                                                                     WPI; 1995-269276/35.
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                                                                                                                                                                                                                                                                                                                                   M.
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inflammatory disease.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and 2C AAQ99892) regions are linked to human constant regions in the C construction of a humanized antibody against VLA-4. The 5' and 3' C ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors CC containing human kappa or gamma-1 constant regions. In the humanized Clight chain, amino acids L45 L49, L58 and L69 in the humanized CC light chain, amino acids L45 L49, L58 and L69 in the humanized CC reposition of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric CC can be used for inhibiting adhesion of a leukocyte to an endothelial CC cell and for treating inflammatory diseases such as multiple CC cerebral traumas, meningitis or encephalitis. The antibodies can corebrating anti-idiotype antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                              Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                  Misc difference
                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                    Chimeric Mus musculus;
                                                                                                                   Region
                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                  acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised alpha-4 integrin antibody 21.6 VL La.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGRDYTFTISSLQPEDIATTYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                     dermatitis; psoriasis; myocardial ischaemia,
                                                                                                                                                                                                                                                                      synthetic
                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                    sapiens;
                                                                /note= "REI framework region
45
                                                                                                                 /note= "21.6
35..49
                            /note= "REI Lys-45 is substd. by Lys of mouse 21.6 VL, important in supporting the
                                                                                                                                                   /label= CDR1
                                                                                                                                                                                  /note= "REI framework region 1"
                                                                                                                                                                                                    /label= FR1
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                   /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                 CDR2 loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                               complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 562; DB 16;
Pred. No. 6.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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22. 21.6 and a modified human REI framework. It can be expressed in a mamplian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephrittis, atopic dematitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see ABW22409) of mouse alpha-4 integrin monoclonal antibody of a sold a modifical human pri framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Fig 6; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "21.6 c 57..88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "REI framework region 4"
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
/note= "21.6 complementarity determining region
97..106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "REI framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leger OJ, Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "REI Leu-103 substd. by Val, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "REI Gln-104 substd. by Glu, of human kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "doot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yednock TA;
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Sequence

106 AA;

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RESULT
AAW22419
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 106;
                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric Mus musculus;
Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised alpha-4 integrin antibody 21.6 VL version La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22419 standard; Protein; 126
                                             21-NOV-1996;
                                                                                   WO9718838-A1
                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                            Peptide
        (ATHE-) ATHENA
                           21-NOV-1995;
                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           digmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips
                                                                                                                                                                                                                                                                                                                                                                         synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
         NEUROSCIENCES INC
                           95US-0561521
                                             96WO-US18807
                                                                                                                                                                             /label= CDR2
/note= "21.6
77..108
                                                                                                                       /label= CDR3
/note= "21.6 |
117..126
                                                                                                                                                                                                                                                                                             /note= "VL version La
21..43
                                                                                                                                                                                                                                                                   /note=
44..54
                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                         /label= CDR1
                                                                                                                                                                                                                                                                                                                                   /label= Leader
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                    /note= "REI framework region 4"
                                                                                                                                                           /note= "REI framework
                                                                                                                                                                      /label=
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                                                                                                                                                                                                                                                                            "REI framework region
                                                                                                                                                                                                                    "REI framework
                                                                                                                                                                                                                                                "21.6
                                                                                                                                                                      FR3
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                                                                                                                                complementarity determining region
                                                                                                                                                                                       complementarity determining
                                                                                                                                                                                                                                               complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 562; DB 18; Pred. No. 6.9e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                        (Claim 25)"
                                                                                                                                                                                                                   region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106;
                                                                                                                                                                                                                                               region
                                                                                                                                                                                        region
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RESULT
AAR81328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The humanised antibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions for the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-297879/27.
N-PSDB; AAT74788.
                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                         02-APR-1996
                                                                                                                                                                                                                                                                                                                                                           AAR81328 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 10; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma, atheroscierosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendig MM,
                                                                                                                                                                                                                                                                              Mouse anti-VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                  AAR81328;
                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                       antibody engineering.
                                                                                                                                                                                                                                                    Humanized antibody; leukocyte
           Region
                                                                Region
                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                            81 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
            50.,56
                                                                35..49
                                                                                                                                                                                  Location/Qualifiers
/label= CDR2
                                       /note=
                                                    /label= FR2
                                                                                          /note=
                                                                                                        /label= CDR1
                                                                                                                                              /note=
                                                                                                                                                            /label= FR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leger OJ,
                           "mouse light region 2"
                                                                                          "mouse light
                                                                                                                                 "mouse light chain variable region 1"
                         region
                                                                              determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS,
                                                                                                                                region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 562; DB 18; Pred. No. 8.1e-37;
                                                                                                                                                                                                                                                      adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dementia,
                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saldanha
                                                                              chain variable region 1"
                                       chain
                                                                                                                                                                                                                                                      molecule; VLA-4; therapeutic;
                                        variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                         framework
                                                                                          complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mus musculus

Location/Qualifiers

"signal peptide"

antibody engineering.

Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

Mouse VLA-4 antibody 21.6 light chain variable region

23-MAR-1996 AAR81326;

(first entry)

Region Region Peptide

> /note= /note=

"framework region 1"

4

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AAR81326
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LCVR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS colling the humanized articles and the statistic of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS colling the humanized articles and the statistic of the mouse 21.6 Ig light chain.
AAR81326 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                            anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                        cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothedial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanised antibodies against VIA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
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                                                                                          61 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106
                                                                                                          61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                             106 AA;
                                                                                                                                                                                                                                                Conservative
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    region 4"
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88.7%;
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Pred. No. 1.1e-32;
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The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They
                                     to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                           anti-idiotype antibodies
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                                                                                                                                                                                                                                                                                                                                                         New humanised antibodies against VLA-4 - used for inhibiting
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117..126
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77..10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VLA-4 reshaped antibody 21.6 light chain variable region
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                   The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule VIA-4. Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VIA-4. The 5' and 3' ends of the
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                                                                                                                                                                 Disclosure; Fig 10;
                                                                                                                                                                                                                                     New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                   Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                             (ATHE-) ATHENA NEUROSCIENCES INC
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55..69
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                                                                                                                                                                                                                                                                                                                                                                                   Saldanha
  (See AAQ99895-98)
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22409 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                               acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                                                                                              atopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-4 integrin mouse MAb 21.6 VL region.
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                                                                             Region
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                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                            dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                            /note= "framework
70..76
                                                                                                                       /note=
77..10
                                     /note= "complementarity
                                                                              /note= "framework
109..116
                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                         /label= FR4
                                                                                                        /label= FR3
                                                                                                                                                                                       /label≖ FR2
                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                         /note= "framework region
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                                                                                                                       .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%;
88.7%;
                                                                                                                                 "complementarity determining
                                                                                                                                                                                                                   "complementarity determining region
            "framework region
                                                                 CDR3
                                                                                                                                                                                                                                                                         FR1
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Pred. No. 1.2e-32;
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                                                                                           region
                                                                                                                                                                            region
                                                    determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
16-SEP-1999
                            WO9946392-A1
                                                                                    Homo sapiens
                                                                                                                             Chemokine; tumour; viral; antigen; fusion protein;
                                                                                                                                                                                        17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                  AAY29913 standard; Protein; 359
                                                                                                                nmune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equivalent to that of naturally occurring human antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uses of humanised alpha-4 integrin antibody -
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N-PSDB; AAT74759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                           and murine scFv38 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 508; DB 18; Pred. No. 1.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (6) human MCP-3 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SDF-1 and HIV gpl20. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays funding interesting inventions. The present sequence represents a fusion protein from the norseent invention.
12-MAR-1998;
                             12-MAR-1999;
                                                                                              WO9946392-A1
                                                                                                                             Synthetic
                                                                                                                                                                                                          Chemokine; tumour; viral; antigen; fusion protein;
                                                                                                                                                                                                                                           Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                           AAY29911 standard; Protein; 361 AA
                                                              16-SEP-1999
                                                                                                                                               ds snw
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                               AAY29911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                              immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                         293 rfsgsgsgrdysfsisnlepediatyyclgydnlytfgggtkleik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                           99WO-US05345
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Pred. No. 1.1e-30;
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                                                                                                                                                                                                            cancer; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen proteins colored fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and HIV gp120; (7) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (7) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human MDC and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SDF-1 and HIV gp120; (8) human SD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH &
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09946392-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Artificial synthetic construct protein SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY29916 standard; Protein; 374 AA.
                                                                                     Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                             12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the present invention.
                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                        98US-0077745
                                                                                                                                                                                                                                                                                                                                                   99WO-US05345
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84.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR60627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and tuman Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and HIV gpl20; (6) human IP-10 and HIV gpl20; (6) human SDF-1 and HIV gpl20; (7) human MDC and HIV gpl20; and HIV gpl20; (8) human SDF-1 and HIV gpl20. The fusion proteins, and nucleotide sequences encoding them, and be used for producing an immune response, e.g. an effector T cell continuous response. They can also be used for treating cancer or treating cor preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. AAY2916 and AAZ21166 to AAZ21168 are sequences given in the SEQ ID LISTING in the present invention but which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV infection \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 117-118; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                     ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR60627 standard; Protein; 128
                                               N-PSDB; AAQ73537
                                                              WPI; 1994-316669/39
                                                                                                 Bigner DD, Carrel S,
                                                                                                                                                                                                                                             14-MAR-1994;
                                                                                                                                                                                                                                                                                                                WO9421294-A
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                   (BIGN/) BIGNER D D. (CARR/) CARREL S.
                                                                                                                                                                                                          19-MAR-1993;
                                                                                                                                                                                                                                                                              29-SEP-1994.
                                                                                                                                  (ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not mentioned further within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                          93US-0033864
                                                                                                                                                                                                                                             94WO-US02724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.8%;
84.9%;
                                                                                                   Zalutsky MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 488; DB 20;
Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Method of treating solid or cystic tumours with antibodies - by administering monoclonal antibody Mel-14, having Fc deleted,

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QΥ
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Best Local
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                                  21-DEC-1989;
21-DEC-1990;
21-DEÇ-1990;
       Jolliffe LK,
                                                                                         WO9109966-A.
                                                                                                              Region
                    (ORTH ) ORTHO PHARM CORP.
                                                              21-DEC-1990;
                                                                           11-JUL-1991.
                                                                                                                           Region
                                                                                                                                         Region
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                                                                                                                                                                    Region
                                                                                                                                                                                  Region
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                             complementarity determining region.
                                                                                                                                                                                                                                                                   variable region;
                                                                                                                                                                                                                                                                                 CD4-specific CDR-grafted light chain.
                                                                                                                                                                                                                                                                                                                          AAR13050 standard; Protein;
                                                                                                                                                                                                                                                                                                27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cystic tumours.
See also AAR60626.
                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of the ME1-14 light chain. The protein monoclonal antibody which can be administered to treat solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                    21 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllmhytstlqpgips 80
                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                               (first entry)
      Zivin RA,
                                89GB-0028874.
90WO-GB02017.
90WO-GB02018.
                                                             90WO-GB02015
                                                                                                                                                       /label
                                                                                                                                                                     /label
                                                                                                              /label= framework region 4
133..234
                                                                                                                                        111..116
                                                                                                                                                                                        /label
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                  /label=
                                                                                                                                               /label= framework
                                                                                                                                                                                                      /labe
                                                                                                                                                                                                                   /label= signal sequence
                                                                                                                                                                                                                                                                    antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                          85.6%;
                                                                                                                            132
                                                                                                                                                             _ CDR 2
                                                                                                                                                                          l= framework region
                                                                                                                                                                                         l= CDR 1
                                                                                                                                                                                                     l= framework region
                                                                                                     kappa constant domain
                                                                                                                                  CDR 3
     Pulito VL,
                                                                                                                                                                                                                                                                   OKT4A; heavy chain; CD4;
                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 481; DB 15;
Pred. No. 1.6e-30;
9; Mismatches 8
                                                                                                                                              region
     Adair
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     JR,
     Athwal
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
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                                                                                                                                                                                                                                                                        RESULT
Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric in reacted with glutathione to produce a mercuric ion coordinate
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AAR78970
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Best Local Similarity
Claim 23; Page 67-68; 106pp; English.
                                             neutralising heavy metals
                                                               New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                N-PSDB;
                                                                                                                                                                    WPI; 1995-275415/36.
                                                                                                                                                                                                                                                               (BION-) BIONEBRASKA
                                                                                                                                                                                                                                                                                                               27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                             27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09520607-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain variable region for monoclonal antibody 23F8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR78970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR78970 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the human kappa constant domain, the signal sequence is derived from murine MAD B72.3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of OKT4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 8; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ12633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-222914/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
||||||||:||
81 rfsgsgsgteytftisslqpediatyycqqydnllftfgqgtklqi 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 diqmtqspsslsasvgdrvtitckaspdinnylnwyqqtpgkapklliyytstlqpgvps 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                AAQ97508
                                                                                                                                                                                                                  Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ12627-Q12632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                               94US-0187407
                                                                                                                                                                                                                                                                                                                                                                95WO-US01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%;
                                                                                                                                                                                                                  Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 475.5; DB 12;
Pred. No. 7.2e-30;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MuLv reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5' end of the CH1 domain of the heavy chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the cariable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97918-Q97510 and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hemocyanin (KLH). Eight hybridomas (LF10, 4A10, 1011, 304, 23ro, 25ro, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T cell activation; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine monoclonal antibody K20 kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR93159 standard; Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F
                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; light chain; kappa; variable region; K20; integrin;
beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1996 (first entry)
                                                               Region
                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   digmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                               /note=
89..94
                                                                                                                                                          /note=
57..88
                                                                                                                                                                                                                                                   /note=
50..56
                                                                                                                                                                                                                                                                                                                                           /note=
35..49
                                                                                                                                                                                                                                                                                                        /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
/label= CDR3
/note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= FR1
                                                                                                                           /label=
                                                                                                                                                                                                                /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.9%;
83.2%;
                                                                                                                                                                                                                                                                            "framework region"
                                                                                           "framework region"
                                                                                                                                                                                    "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 471.5; DB 16; Length 107; Pred. No. 7.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23F8, 2D5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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RESULT
                                                                                                                                                                                                                   AAR06252
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanisation process, the complementarity immunosuppressant. In the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanisation of non-human immunoglobulin variable regions prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1994;
                                  01-AUG-1990
                                                                                                                              Variable region of murine AHT 107 light chain.
                                                                                                                                                      10-DEC-1990
                                                                                                                                                                                                       AAR06252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 2A; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEINE PERFORMANCE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-1996
                                                          EP380068-A.
                                                                                                        Interleukin-2 receptor; IL-2;
                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                               1 diqltqspsslsaslggkvtitckasqdinkyiawyqhepgkgprllirytsklesgips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1996-162083/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervoni MF,
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94FR-0010858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94FR-0010858
           90EP-0101351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= J_kappa1
                                                                                                                                                                                                      protein; 128
                                                                                                                                                                                                                                                                                                                                                                         82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lefranc
                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                              Score 465; DB 17;
Pred. No. 2.3e-29;
0; Mismatches 10;
                                                                                                          tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΜP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDICALE
                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
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                                                                                                                                                                                                                                                                                                                                                               0;
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Search completed: May 7, 2002, 12:22:25 Job time: 246 sec
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                                                                                                                                                                    Query Match
Best Local S
Matches 82
                                                                                                                                                                                                                                                          MAbs comprising mouse CH and CL constant regions whith human variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce Abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                    Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                              Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                     Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ05556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1989;
24-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-232892/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR THERAPEU.
                                                          y Match 81.9%; Score 460.5; DB 11; Length 128; Local Similarity 76.6%; Pred. No. 6e-29; hes 82; Conservative 18; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-0441702.
89US-0301216.
                                                                                                                                                                  1;
                                                                                                                                                                  Gaps
                                                                                                                                                                  1;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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US-08-561-521-7
PCT-US95-01219-7
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PCT-US95-01219-15
PCT-US95-01219-15
PCT-US95-01219-15
PCT-US95-01219-15
US-08-339-582-4
US-08-888-366-22
US-08-235-838-16
US-08-465-4738-11
US-08-662-725-29
US-08-662-725-29
US-08-662-725-29
US-08-675-1521-8
PCT-US95-01219-8
PCT-US95-01219-8
PCT-US95-01219-8
US-08-437-6428-17
PCT-US93-07832-17
US-08-437-6428-18
PCT-US93-07832-18
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PCT-US93-07832-18
US-08-437-6428-18
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Query Match

Best Local Similarity

100.0%; 100.0%;

Score 562; DB 2; Pred. No. 1e-45;

Length 106;

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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYNAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/I
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                  APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                     TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 90.4%; Score 508; DB 2; Length 106; Local Similarity 88.7%; Pred. No. 1.1e-40; hes 94; Conservative 6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:

94105

COUNTRY:

USA

San Francisco California

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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 88.7%;
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FILING DATE: 25-JAN-1995
                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                            COUNTRY:
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APPLICATION NUMBER: US/08/561,521
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Pred. No. 1.1e-40;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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APPLICANT:
APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William L. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
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                                                                                                                                                                                                                                               FILING DATE
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                                                                                                                                                                                                                           CLASSIFICATION: 424
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 CHARACTERISTICS:
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                                     415-543-5043
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Pred. No. 1.3e-40;
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Best Local Similarity
watches 94; Conserva
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-15
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TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bendig,
APPLICANT: Leger,
APPLICANT: Saldanha
APPLICANT: Jones,
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                             TELEPHONE: 415-543-9600
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 25-JAN-1994
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FILING DATE: 25-JAN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Jones, S. Tarran
                                                                   Conservative
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Leger, Olivier J.
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88.7%;
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88.7%;
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                                                                  Score 508; DB 5; Length 126; Pred. No. 1.3e-40; 6; Mismatches 6; Indels
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RESULT 9
US-08-339-582-4
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                                                                       Sequence 4, Application US/08339582 Patent No. 5558852
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Best Local Similarity
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                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                   APPLICANT:
                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humanized Antibodies Agrille Of INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                        94; Conservative
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amino acid
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Zalutsky, Michael R. Carrel, Stefan
                                     Bigner, Darell D
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                                                                                                                                                                                                                                                                                                                                    90.4%; Score 508; DB 5; Length 126;
88.7%; Pred. No. 1.3e-40;
ative 6; Mismatches 6; Indels
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US-08-888-366-22
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                                                                                                                                                                                                                                                 Sequence 22, Application US/08888366

Patent No. 5972656

Patent No. 5972656

Patent INFORMATION:

APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.

APPLICANT: Wagner, Fred W.

TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
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                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 85.6%;
Local Similarity 84.0%;
                                                                                                                               COUNTRY:
                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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90 South 7th Street, 3100 No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16,
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Best Local Similarity
Matches 89; Conserv
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CCOmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            APPLICANT: Zwickl, TITLE OF INVENTION: TITLE OF INVENTION:
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LENGTH: 107 amino acids
TYPE: amino acid
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FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 08/187,407
                                                                                                                         ZIP: 10532
                                                                                                                                        COUNTRY:
                                                                                                                                                            STATE:
                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                           STREET:
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APPLICATION NUMBER:
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                                                                                                                                                                          Hawthorne
                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                  Zwickl, Markus
                                                                                                                                                                                                                                                                                                                 Hardman, No.
                                                                                                                                                                                                                                                                                                                                     Groner, Bernd
                                                                                                                                                                                                                                                                                                                                                    Harwerth,
                                                                                                                                                                                                                                                                                                                                                                    Hynes, Nancy E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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83.2%;
                                                                                                                                                                                                                                                            Recombinant Antibodies Specific for a Growth Factor Receptor
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 US/08/235,838
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Pred. No. 2.7e-37;
"""matches 8;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
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REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 91-810079.3
                    FILING DATE: 31-JAN-1992
PRION APPLICATION DATA:
APPLICATION UMBER: GB 9
FILING DATE: 05-FEB-1991
                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
Filing DATE: 31-JAN-1992
                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                           APPLICATION NUMBER: US/08/465,473B FILING DATE: 5 June 1995
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                         5 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.9%; Score 460; DB 1; 80.2%; Pred. No. 2.3e-35;
                                         GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/828,832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                 TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TYPE: amino acids
TYPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                              FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                 FILING DATE: TI
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hawthorne
STATE: New York
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                                                 TELEPHONE:
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wels, Winfried S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harwerth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIBA-GEIGY Corporation
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                                                                                                                                                                                                                            31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.9%; Score 460; DB 2; Length 637; 80.2%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ina-Maria
                                                                                                                                                                                                                                                                                                                       US/08/235,838
                                                                                                         36,129
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                                                                                           4-18518/A/CIP/CONT
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-838-11
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-08-465-473B-11
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                                                                                                         TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wels, Winfried
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-w
                                                                                                                                             REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/828,832 FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
             MOLECULE TYPE: protein
                                                                                                                                                                                                     FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfelffer, Hesna J.
REGISTRATION NUMBER: 22,0
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 5
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08 FILING DATE: 5 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Summit
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mes 84; Conserv
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                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                     LENGTH:
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                                             d: 241 amino acids amino acid
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                                                                                                                                                                                                                                                                                    GB 91-810079.3
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                                                                                                                                                                                     4-18518/A/CIP/CONT2
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Query Match

81.0%;

Score 455;

DB 2;

Length 241;

Matches

Conservative

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Mismatches

Indels

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                                                                      ; ORGANISM:
US-08-602-725-29
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
EXTINC TARE: GB 9317423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                       FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9317423 FILING DATE: 21-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                       HYPOTHETICAL: NO
                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 02-FE
                                                                                                                                                                                                                                                                                                                                NAME: SADOFF, B.J.
REGISTRATION NUMBER: 360
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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BATES, PAUL A
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Match
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Copyright (c) 1993 - 2000
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Q9u192 homo sapien
Q99la6 mus musculu
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Q9rla4 mus musculu	Q9R1A4	11	437	35.3	263.5	44
Q9ul84 homo sapien	Q9UL84	4	122	35.6	265.5	43
Q9u191 homo sapien	Q9UL91	4	118	35.9	267.5	42
Q9n0w4 oryctolagus	Q9N0W4	6	124		269.5	41
Q9n0w6 oryctolagus	9M0M6	σ	124	36.4	271.5	40
Q9u171 homo sapien	Q9UL71	4	121	36.9	275	39
Q99m22 mus musculu	Q99M22	11	479		279	38
Q9u193 homo sapien	Q9UL93	4	116	37.4	279	37
	Q9Y509	4	147	37.7	281.5	36
Q99ng4 mus musculu	Q99NG4	11	121	38.1	284.5	ω 5
_	Q9UL88	4	131		285	34
Q9u190 homo sapien	Q9UL90	4	113	38.9	290	33
Q9hccl homo sapien	Q9HCC1	4	112	39.1	291.5	3 2
Q9bu10 homo sapien	Q9BU10	4	597	39.4	294	31
Q9u173 homo sapien	Q9UL73	4	119	39.4	294	30
homo	Q9UL72	4	118		294.5	29
Q9bqb8 homo sapien	Q9BQB8	4	597		295	28
Q9bual homo sapien	Q9BUA1	4	120	40.3	301	27
095973 homo sapien	095973	4	150		302.5	26
Q9qyf0 mus musculu	Q9QYF0	11	298		322.5	25
_	Q9UL89	4	116		324.5	24
Q9z1c6 mus musculu	Q921C6	11	117		338	23
Q99ka4 mus musculu	Q99KA4	11	487		340.5	22
Q9u195 homo sapien	Q9UL95	4	125		343	21
Q9j183 mus musculu	Q9JL83	11	110	46.7	348.5	20

### ALIGNMENTS

Q99L31 PRELIMINARY; PRT; 46
Q99L31;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequer
01-JUN-2001 (TrEMBLrel. 17, Last annota
SIMILAR TO RIKEN CDA 1810060009 GENE.

sequence update) annotation update)

468 AA

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NCBI\_TaxID=10090;

SEQUENCE FROM N.A.

Mus musculus (Mouse)

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Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
EMBL; BC003878; AAH03878.1; -.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
Q99L25 PRELIMINARY;
Q99L25;
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                 121
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Similarity 81.4%;
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Pred. No. 2.2e-51
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Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B., "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.", submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JL85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -. nrqRRqR7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IYYG-YGLYYFDYWGQGTTITV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
88 TITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                                             28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                1 ABLVKPGASVKLSCTASGENTEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
                                                                                                                                                                                                                                                 PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFGAREG- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YYGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS 120
                                                                                                                                                                                                                                     SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                        109 AA;
                                                                                                                 Conservative
                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                          109
                                                                                                                                                                                        11944 MW;
                                                                                                                              64.3%;
80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                8;
                                                                                                                            Score 480; DB 11.
Pred. No. 3.8e-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 494.5; DB Pred. No. 8e-42;
                                                                                                                                                                                       DFE615FE6CED4EDE CRC64;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA
                                                                                                                                         DB 11; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hassegawa Y., Kawaji H., Kohtsuki S.,
RA Havashiraki Y., Storch
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_MRC; UNKNOWN_1.
SMART; SM00410; IG_MRC; UNKNOWN_1.
SMART; SM00406; IG_MRC; UNKNOWN_1.
SMART; SM00410; IG_MRC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 1810060009RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1924014; 1810060009Rik.
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01-JUN-2001
121 -- DYDWFA--YWGQGTLVTV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21085660; PubMed=11217851;
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                                        121 YGNYGYYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810060009RIK
                                                                                       61
                                                                                                                               61
                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                  1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRP
                                                                                                                                                                                    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR-----GAVVFDYWGQGTALTV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                              GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY
                                                                                                                      EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK007918; BAB25349.1;
                                                                                                                                                                                                                                                 64.1%; Score 478; DB 11;
Similarity 67.1%; Pred. No. 3.7e-40;
19; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig_c1
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                                                                                                                                                                                                                                                                                                                                                         9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                           Length 473;
                                                                                                                                                                                                                                                     Indels
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Best Local 9
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EMBL; BC00
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O99LC4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                  O9QXE9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                   Q9QXE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                  NON_TER
                                                                                                                                                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                     SEQUENCE
                                                                                                                                                                                           EMBL; AJ225174; CAB65237.1;
                                                                                                                                                                                                                                Clemens A., Rademaekers A., Specht C., Koelsch E.; submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
            20 EVQLQQSGAELVKPGASVKLSCTASGENIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY
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                                                                                                                                                                                                                   SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y-SYDLFA--YWGQGTLVTV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tted (FEB-2001) to the EMBL/GenBank/DDBJ databases BC003435; AAH03435.1; -.
NCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                 Similarity
                                                                                                     117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                      13000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.0%;
                                                 55.2%;
                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                     Score 412; DB 11;
Pred. No. 3.1e-34;
l4; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 425.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                      CDDE2AF84D499734 CRC64;
                                                                                                                                                                                                                      AND MAJOR HISTOCOMPATIBILITY
                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3e-35;
                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 463;
                                        6,
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RESULT
Q9Z1C4
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                                                                                                                                                                                                                                                                  Q9QXF0
                                                                                                                                                                                                                                                                                                 RESULT
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Best Local S
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Q9Z1C4;
                                                                                          O9QXFO:
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelial cells.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                           Q9QXF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgG2/G4 constant regions block human leukocyte binding
NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 V 115
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                                                                                                                                                                                                                                                                                                                                                                                 113
                                                                                                                                                                                                                                                                                                                                                                                                                                 137 SVTV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE---GYYGNYGVYAMDYWGQGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                 TLTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U78801; AAD00293.1;
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118 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13036 MW;
                            Rodentia;
                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 388.5; DB 1
Pred. No. 7.5e-32;
                            Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                 117
                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                               Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118;
                                  Murinae; Mus
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Best Local
                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                           Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                              SEQUENCE
                                                                                                                                                                          NON_TER
                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                       EMBL; AF206029; AAF69327.1;
                                                                                                                                                                                                                                                                                                                                                    STRAIN=DBA/2;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JL77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
90 TADŢSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                         30 LVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKATI 89
                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYY-----FDYWGQGTTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                              3 LVRPGASVKLSCKASGYTFTSSWMHWAKQRPGQGLEWIGEIHPNSGHTNYNEKFKGKATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                  SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ225171; CAB65236.1; -.
                                                                                                       Similarity
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                                                                                                                                                           110 AA;
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117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                              TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                          110
                                                                                                                                                        12138 MW; 2EDE81FB5862C9AF CRC64;
                                                                                                   51.4%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%;
63.1%;
                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                     Score 383.5; DB 1
Pred. No. 2.2e-31;
5; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA.
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                                                                                                              DB 11; Length 110;
                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                      Indels
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                                                                                     Gaps
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                                                                                     1;
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RX KEWAIN-2108566; PubMed-11217851;
RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch R.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki V., Storkida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local Similarity
Q9JL75 PRELIMINARY;
Q9JL75;
01-OCT-2000 (TrEMBLrel. 15,
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1700110L11, FULL INSERT SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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STRAIN=C57BL/6J; TISSUE=TESTIS;
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01-JUN-2001
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                                                                                                                                                                                                                                                       61 DGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR 104
                                                                                                                                                                                                                                                                                                                       74 NGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPA 73
                                                                                                                                                                                                                                                                                                                                                                                                   1 MTGVHSQVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPG 60
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.9%; Score 380; DB 1 70.2%; Pred. No. 5e-31;
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       Created)
                                                                               PRT;
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SEQUENCE
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                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                       01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autolamune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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IPR003596; Ig_v.
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                                                                                                                              IPR003006;
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114 AA;
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12829
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Rodentia;
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            50.3%;
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 21;
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Pred. No. 1.1e
18; Mismatches
            Score 375.5;
Pred. No. 1.
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Sciurognathi; Muridae;
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No. 1.5e-30;
smatches 21;
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hes 18;
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; Murinae; Mus
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                                                                                                                                                                                                                                                                          Murinae;
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RESULT
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Q99LA6
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Best Local
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                                                                099LA6;
01-JUN-2001 (TrEMBLrel. 17, Creat
01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 17, Last
UNKNOWN (PROTEIN FOR MGC:6319).
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SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UL92;
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                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
SEQUENCE
                       NCBI_TaxID=10090;
                                                          Mus musculus (Mouse)
                                                                                                                           Q99LA6
                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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fetus.":
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LTVDKSSSTAYWQLSSPTSEDSAVYYCARSNYYGS-SLYYFDYWGQGTTLTV 112
                                                                                                                                                                                                           WGQGTSVTV 140
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                                                                                                                                                                                                                                                                                          EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLVRPGASVKISCKASGYSFTSYWMHWVKQRPGQGLEWIGMIDPSDSETRLNQKFKDKAT
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                                                                                                                                                                                    WGQGTLVTV 122
                                                                                                                                                                                                                                                        DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAM------DY 131
                                                                                                                                                                                                                                                                               EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
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                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    124
124 AA;
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                                                                                                                             PRELIMINARY;
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; 13580 MW;
                                 Chordata;
Rodentia;
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56.6%;
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                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                                  Score
                                 Craniata; Vertebrata; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                     1BAAACBD96ACD2A2 CRC64;
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                                                                                annotation
                                                                                           sequence update)
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                                                                             update)
                                    Muridae;
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                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION
                                    Murinae;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation:
Ig64 monoclonal antibody derived from a hemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003495; AAH03495.1; -
SEQUENCE 484 AA; 52567 MW; 8EAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor.";
Blood 92:496-506(1998).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-101 (TrEMBLrel. 17, Last annotation update)
11G WH PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GVYAMDYWGQGTSVTV 140
                                                121 YGNYGYYAMDYWGQGTSVTV 140
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                                                                                                Local Similarity tes 67; Conserv
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                                                                                                                                                                                                             1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                         1 MKCSWVMFELMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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---- PPDAFDIWGQGTMVTV 134
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150 AA;
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nilarity 49.3%;
Conservative 28
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150
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                                                                                                                                                                                                                                                                                                                         24; Mismatches 38;
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Pred. No. 4e-29;
8; Mismatches 39; Indels
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Search completed: May 7, 2002, 12:31:42 Job time: 628 sec

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OM protein - protein search, using sw model
                                                       Run on:
May 7, 2002, 12:23:47; Search time 37.68 Seconds (without alignments) 214.291 Million cell updates/sec
                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: Sequence: US-09-155-739-7 562

1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 segs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	5	4	ω	2	_	No.	Result
412	412.5	413.5	414	•	415.5	418.5		419.5	•	•	N	•	•	435.5		9	439.5	440	440.5	443	443.5	443.5	446.5	452	463.5	478	479	488	Score	
	73.4			73.8		٠	٠	74.6				٠	76.4				78.2	•			78.9			ō	82.5	5	85.2	9		% Query
106	108	108	124	131	109	123	108	108	108	125	107	127	110	108	108	107	107	94	107	103	129	108	107	97	125	106	104	104	Length	ı
2	2	_	N	N	N	N	_	_	_	2	2	2	N	2	Н	2	N	N	N	Ν	2	μ	ν	N	2	N	N	Ν	DB	
PC2397	B49047	K1HUSW	S40336	S40352	S31998	S40331	K1HURY	K1HUAG	K1HULY	S40333	S36275	S40367	S44118	I39154	K1HUAU	PL0271	PL0269	E33730	PL0272	S26332	S52789	K1HURE	PL0270	PH1064	S09365	C33936	S26329	S26330	ID	
4		_	chain V-	Ig kappa chain V-J	_	_	kappa chain V-	_	chain V-	Ig kappa chain V-J			_	kappa chain	kappa chain V-	kappa chain	-	kappa		Ig light chain V r			kappa chain V	Ig light chain V r		chain V		ain V	Description	

410.5 · 73.0 108 2 S44122 II Kappa 410.5 · 73.0 109 2 S31981 II Kappa 410.5 · 73.0 109 2 S31981 II Kappa 410.5 · 73.0 109 2 S31981 II KAPPa 410.5 · 72.9 129 1 KIHUWR II KAPPa 410.5 · 72.9 129 1 KIHUWR II KAPPa 410.5 · 72.7 10.8 1 KIHUWE II KAPPa 410.5 · 72.7 13.9 2 S40365 II KAPPa 410.5 · 72.7 13.9 2 S40365 II KAPPa 410.5 · 72.2 11.7 2 S466371 II KAPPa 410.5 · 72.1 110.8 2 S30521 II KAPPa 410.5 · 72.1 110.8 2 S30521 II KAPPa 410.5 · 72.1 110.8 2 S30521 II KAPPa 410.5 · 72.1 110.8 2 S30521 II KAPPa 410.5 · 72.1 110.7 2 S30521 II KAPPa 410.5 · 71.8 II CONTROL SAPPA 410.5	45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30
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	K1HUHU	S42263	S43528	S11240	S36264	PH1063	S40334	S30521	S46371	A49134	S40365	K1HUWE	K1HUAR	K1HUWK	S31981	S44122
chain V chain F chain F chain V chain V chain V chain V chain V chain V chain V chain V chain V chain V chain V chain V chain V	Ig ka	Ig kapı	Ig kapp	Ig kappa			kappa	kappa	kappa	kappa	kappa	kappa	kappa	kappa	kappa	

## ALIGNMENTS

RESULT 2  \$26329  If kappa chain V region - mouse C; Species: Mus musculus (house mouse) C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C; Accession: \$26329 C; Accession: \$26329 R; Stark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991 A; Title: Antibodies that are specific for a single amino acid interchange in a protein pr	Query Match  86.8%; Score 488; DB 2; Length 104;  Best Local Similarity 85.6%; Pred. No. 1.3e-35;  Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60  1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60  2 Oy 61 RFSGSGSGRDYTFTISSLQPEDIATTYCLQYDNLWTFGGGTKVE 104  1	RESULT 1 \$26330 If kappa chain V region - mouse C; Species: Mus musculus (house mouse) C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C; Accession: \$26330 R; Stark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991 A; Fitle: Antibodies that are specific for a single amino acid interchange in a protei A; Feference number: \$26309; MUID:91341421 A; Accession: \$26330 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-104 <sta> A; Cross-references: EMBL: X59185; NID:952316; PIDN:CAA41895.1; PID:91334063 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology <imm></imm></sta>
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Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
N;Feddersen, R.; van Ness, B.
                                                                                                                                                                                                            C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S09365
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                                                          QΥ
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A; Residues: 1-125 <FED>
                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S09365
                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segral, Reference number: S09365; MUID:90098844
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                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene A; Reference number: A33936; MUID:89282831
A; Accession: C33936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                   Best
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Best Local
    18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77
                                                                                                                                 POCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RESGSGSGRDYSESISNLEPEDIATYYCLQYDNLYTEGGGTKLE 104
                               1 DIÒMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                           99;
                                                                                                                            Similarity
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                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                            82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.1%; Score 478; DB 2; 83.0%; Pred. No. 9.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                              Pred.
                                                                                                                                                  Score 463.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 479; DB 2; Length 104; Pred. No. 7.8e-35;
                                                                                                        Mismatches
                                                                                                                              No. 2e-33;
                                                                                                                                               DB 2;
                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 106
                                                                                                                                               Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                    Indels
                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                    Gaps
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V
                                                     В
                                                                                                                                                                                                                                               F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                          F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                      \begin{array}{ll} F; 16\text{-}90\text{/Domain: immunoglobulin homology} < \text{IMM} > \\ F; 24\text{-}34\text{/Region: complementarity-determining 1} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-23/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-107 < SHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: PL0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                              Match 79.4%;
Local Similarity 79.4%;
                                           1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-ONA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Experimental source: B cell, strain [NZB x NZW]F1 C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
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                                                                                      Score 446.5; DB 2
Pred. No. 5.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 452; Db 2, Pred. No. 1.6e-32;
                                                                 Mismatches
                                                                                                                  DB 2;
                                                          10;
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                                                             Indels
                                                                                                                     Length 107;
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                                                       Gaps
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Ig kappa chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: $52789

R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, submitted to the EMBL Data Library, March 1995

A;Description: Light chain V region gene usage restriction and peculiarities in A;Reference number: $52789

A;Reference number: $52789

A;Accession: $52789

A;Accession: $52789

A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Residues: 1-129 <ROC>
A;Residues: 1-129 <ROC>
A;Residues: FARCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the A;Reference number: A90392; MUID:76039968
A;Contents: annotation; X-ray crystallography, 2.0 angstroms C;Comment: This is a Bence Jones protein.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-108 <PAL>
A; Note: the C region of this chain has the Inv (1,2) marker R; Epp, 0.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstaendige Aminosaeuresequenz des Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
C;Accession: A91663; A01873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                  A;Cross-references: EMBL:x85995; NID:g758588; PIDN:CAA59987.1; PID:g758589 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;38-112/Domain: immunoglobulin homology <IMM>
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A; Map position: 2p12
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                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                        Similarity
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  Conservative
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                      78.98;
79.48;
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81.1%;
  10;
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                      Score 443.5; DB Pred. No. 1.1e-31
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Pred. No. 9.4e-32;
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    Mismatches
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                                               Length 129;
  Indels
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                        F;98-107/Region:
                                                 F;89-97/Region:
                                                                     F;57-88/Region:
                                                                                           F;50-56/Region:
                                                                                                                    F;35-49/Region:
                                                                                                                                           F; 24-34/Region:
                                                                                                                                                                   F;16-90/Domain:
                                                                                                                                                                                          F;1-23/Region: tramework
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A; Molecule type: mRNA
A; Residues: 1-103 <ST2>
A; Residues: 1-103 <ST2>
A; Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                       A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecular L
C; Superfamily: immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V region (anti-DNA, 688VK) - mouse (frachent) C;Speckes: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change C;Accession: PLO272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: x59187; NID: g52318; A; Note: the sequence of residues 1-8 and the
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C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: Ig kappa chain V region
                                                                                                     A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
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Best Local :
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Exp. Med. 174, 613-624, 1991
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77.7%;
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Pred. No. 9.9e-32;
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complementarity-determining complementarity-determining
framework 3

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framework 2

complementarity-determining immunoglobulin homology < IMM>

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Gaps

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F:57-88/Region: framework s
F:89-97/Region: complementarity-determining
F:98-107/Region: framework 4
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A; Accession: PL0269
A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
C; Superfamily: immunoglobulin V region; imm C; Keywords: heterotetramer; immunoglobulin F; 1-23/Region: framework l
F; 16-90/Domain: immunoglobulin homology <IN
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PLO269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
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A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unl A;Reference number: A33730; MUID:89367325
A;Accession: E33730
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A; Residues: 1-94 <LAW>
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
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                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASLGGKVTTTCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS
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                                                                                                                                                                                                            complementarity-determining 2
framework 3
                                                                                                                                                                                                                                                                                  complementarity-determining 1
framework 2
                                                                                                                                                                                                                                                                                                                                                             immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.3%;
86.2%;
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78.5%;
                       78.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 440.5; DB Pred. No. 1.7e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 440; DB 2;
Pred. No. 1.6e-31;
                       Score 439.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 107;
                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                   2;
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                   Length 107;
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                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-108 <SCH>
A; Residues: 1-108 <SCH>
A; Note: the C region of this chain has the Inv (3) marker
R; Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager,
Biophys. Struct. Mech. 1, 139-146, 1975
A; Title: The structure determination of the variable portion of the Bence-Jones
A; Reference number: A90729; MUID:77022433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
                                                   R;Steiner, V.; Chang, J.Y. FEBS Lett. 222, 6-10, 1987
                                                                                                                 A; Contents: annotation; X-ray crystallography A; Note: the structure of the V region was determined by molecular replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1
A;Title: Die Primaerstruktur einer monoklonalen
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R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein R;Shlomchik, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; Mascelli, M.; M
A;Title: Chemical modification of the carboxyl groups of protein substrates ephances
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A91653; MUID:72189444
A;Accession: A91653
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F;57-88/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
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A; Accession: PL0271
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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Gaps

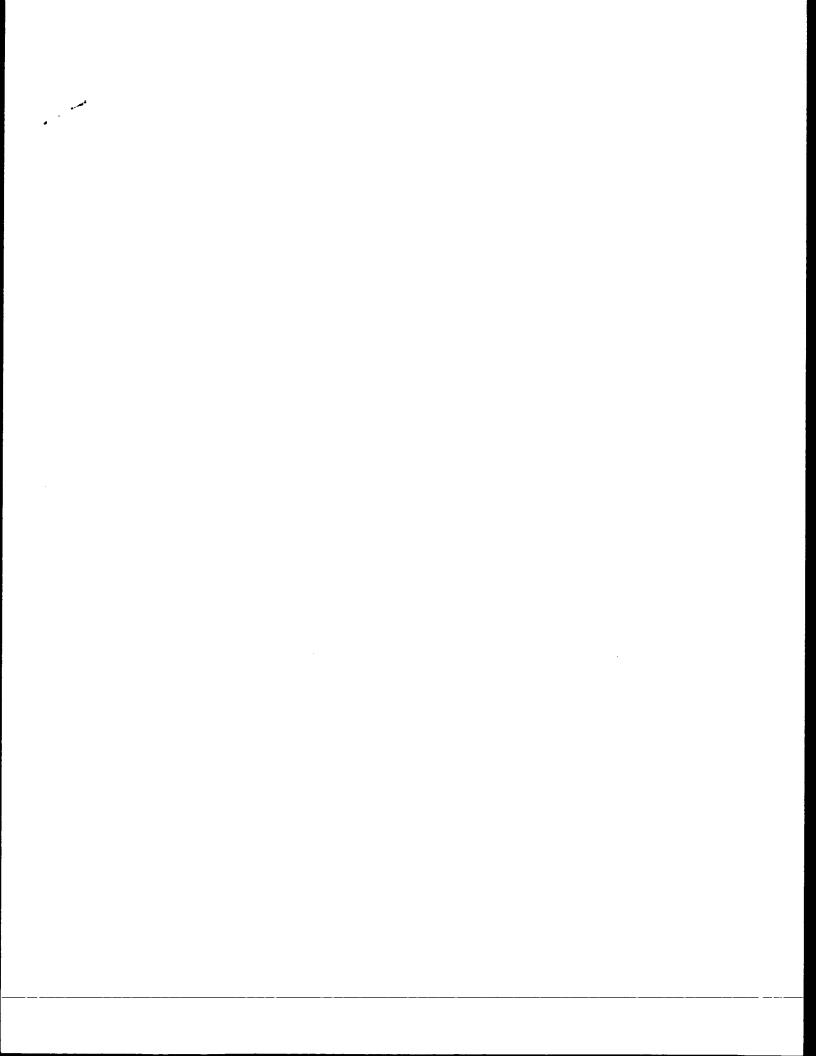
methods

P.,

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I39154

I39154

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C; Accession: I39154
R; Schormann, N; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A; Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A; Reference number: I39154; MUID:96003804
A; Accession: I39154
A; Status: precliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-108 <RESS-
A; Cross-references: EMBL:U31344; NID:9344925; PIDN:AAA79238.1; PID:9944926
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S02572; MUID:88005152
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V reglon; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
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Search completed: May
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Best Local S
Matches 85
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79.4%;
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Pred. No. 2.1e-31;
8; Mismatches 13;
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OM protein - protein search, using sw model
                                                         Run on:
May 7, 2002, 12:32:34; Search time 21.92 Seconds (without alignments) 177.303 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Title:
Perfect score:
Sequence:

US-09-155-739-7
562
1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

419.5 419.5 419.5		108 108 108		KV1B_HUMAN KV1A_HUMAN KV1A_HUMAN KV1P_HUMAN	P01594 P01605 P01593 P01593	homo
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0		107	1	KV1D_HUMAN	p01596	
	•	108	۲	KV1R_HUMAN	P01610	
	•	108	ш	KV1H_HUMAN	P01600	
	•	108	-	KV1F_HUMAN	P01598	homo
•	•	108		KV1V_HUMAN	P04430	homo
	•	801	- ب	KV1K_HUMAN	P01603	homo
•		108 108	<u> </u>	KVLE_HUMAN	P01597	
	•	100	4 د	KVIL_HUMAN	P01504	
		108	٠,	KV1C HUMAN	P01595	homo
	•	108	Ľ	KV1G_HUMAN	P01599	
٠	•	129	۳	KV1X_HUMAN	P04432	
٠	•	108	щ	KV1S_HUMAN	P01611	
•		134	ب	KV4C_HUMAN	P06314	
٠.	•	108	₽	KV5J_MOUSE	P01643	_
36	•	117	÷	KV1J_HUMAN	P01602	home
66.	•	128	μ.	KV5E_MOUSE	P01637	mus musculu
36	•	133	ب	KV4B_HUMAN	P06313	homo
	•	108	μ,	KV50_MOUSE	P01648	mus musculu
ω	•	108	۳	KV5N_MOUSE	P01647	mus
σ	64.4	109	μ,	KV1T_HUMAN	P01612	home
σ	•	117	۳	KV1I_HUMAN	P01601	
٠	•	108	۲	KV5K_MOUSE	P01644	
•	•	108	_	KV5M_MOUSE	P01646	mus
•	•	108	٠	KV5L_MOUSE	P01645	mus musculu
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P01624 homo sapien									P04207 homo sapien		

# ALIGNMENTS

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<b>⊔</b>	03006 03596 03596 19; ; IGv V re V re 1	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTRO MEDLINE-76039968; PubMed=1182131; EDP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Schiffer M., EPP O., Lattman E.E., Lattman E	MEDLINCE. SEQUENCE: , Hilschmann N.; Palm W.; Hilschmann N.; "The primary structure of a kappa-type L-chain, subgroup and characterization of the sequence of the protein; a c three-dimensional structure combling site."; Hoppe-Seyler's Z. Physiol. C [2]	TANDAR  01, 01, 38,
	WHC.  Bence-Jones protein; 3D-structure. FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  MEDILINE-76039968; PubMed-1182131;  EDP O., Lattman E.E., Schiffer M., Huber R., Palm W.;  EDP O., Lattman E.E., Schiffer M., Huber R., Palm W.;  "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";  Biochemistry 14:4943-4952(1975).  -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  MARKER.  -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  PIR: A01873; KIHURE.	MEDLINE-76023758; PubMed=809329;  Balm W., Hilschmann N.;  Palm W., Allschmann N.;  "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";  Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).	Created) Created) Last sequence update) Last annotation update) LON REI. cordata; Craniata; Vertebrata; Euteleostomi; imates; Catarrhini; Hominidae; Homo.

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ASSP; PO16v,
InterPro; IPRU.
InterPro; IPRU03559v,
IPfam; PF00047; ig; 1.

PS SMART; SM00406; IGv; 1.

FIMMUNOGIOBULIN V region; Bence-
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S0 56
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 (Rel. 38, Last annotation updat
16 KAPPA CHAIN V-I REGION AU.
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STRAND
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                                                                                                                                                                                                                                                                    Schiechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                          Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
                                                                                                                                                                                                                                                                                                           MEDLINE=72189444; PubMed=5028201;
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81.1%;
                                  Bence-Jones protein.
FRAMEWORK 1.
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Pred. No. 5.7e-40;
               FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
        FRAMEWORK 3.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION LAY.
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-i- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra J.D., Klapper D.G.;
"Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
                                                                                      Local
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                                                  1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                               GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS
                           DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
                                                                             81;
                                                                                        Similarity
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79.4%;
                                                                                                                                           11834 MW; 739993A95431434A CRC64;
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                                                                             11;
                                                                          Score 421.5; DB 1
Pred. No. 1.2e-37;
1; Mismatches 13
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Pred. No. 1.5e-39;
                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                          FRAMEWORK 3
                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING
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AC P01593
AC P01593
AC P15-JUL
DT 21-JUL
RX MEDLIN
RX MEDLIN
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P01608;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION ROY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The amino acid sequence of a kappa type Bence-Jones protein. complete sequence and the location of the disulfide bridges."; Biol. Chem. 244:3550-3560(1969).
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InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 244:3550-3560(1969).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION AG.
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MEDLINE=68362076;
Hilschmann N.;
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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                   PubMed=5595110;
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Primates;
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Primates;
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Pred. No. 1.9e-37;
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COMPLEMENTARITY-DETERMINING
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FRAMEWORK 1.
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                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae,
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                                                                                                       Hominidae;
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    RESULT 6
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Steinmetz-Kayne M., Suter L., V
(In) Franck F., Shugar D. (eds
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Stevens F.J., Westholm F.A., Panagiotopoulos N., Popp R.A., Solomon A.; "Characterization and preliminary crystallographi related fragment of the human kI Bence Jones prot
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                                                                                                                                              Biochemistry
                                                                                                                                                                 structural origin of altered domain
light-chain dimers.";
                                                                                                                                                                                                      MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Alnsworth C., Bruenger A.T.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous pro
                                                                                                                                                                                                                                                                                        SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=81267384;
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Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                 FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
                                                                                                                                       COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
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                      BY SIMILARITY.
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                                                        FRAMEWORK 4.
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InterPro; IPR003596; Iq_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                   PIR; A01883; K1HUWK. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klobeck H.G., Combriato G., Zachau H.G.; "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
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23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS
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0; Mismatches
                                                                          Score 409.5;
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Pred. No. 8.1e-37;
                                                                                                                                         FRAMEWORK 4.
BY SIMILARIT
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Best Local :
Goni F., Frangione B.;
Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal I
"Amino acid sequence of the Fv region of a human monoclonal I
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
                                                                                                                                                                                                                                                                                                  protein.";
Eur. J. Biochem. 49
-1- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
CARBOHYD 28 28
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Milstein C.P., Deverson E.V.;
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Mammalia; Eutheria; Primates;
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION CAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01596;
21-JUL-1986
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                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                    \mathbf{I}\mathbf{G}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                       Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
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                                                                                                                                                                                                                                                                                    KAPPA CHAIN V-I REGION WEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A01864; K1HUAR.
; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESGSGSGTDETLTISSLQPEDSATYYCQQSYSTLITEGQGTRLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESGSGSGTDETLTISSLZPBBEATYYCQQYNTFFTFGPGTKVDIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003006; Ig_MHC.
IPR003596; Ig_v.
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107
107
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                                                                                                                                                                                                                                                             (Human)
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S: THE C REGION OF
                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.8%;
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Pred. No. 2
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Catarrhini; Hominidae
                                                                                                                                                                                                                       Catarrhini; Hominidae;
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                                                                                                                                                                                                                                         Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                           Euteleostomi;
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KV1H_HUMAN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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DOMAIN
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DISULFID NON_TER
                                    DOMAIN
DOMAIN
                                                                                                                                                   Hoppe-Seyler's Z. Physiol.
-!- MISCELLANEOUS: THE C RI
-!- MISCELLANEOUS: THIS IS
                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01876; K1HUWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WIT
                                                                                                                                                                                               Watanabe S., "The primary
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                         P01600;
                            DOMAIN
                                                                                           Pfam; PF00047; ig; SMART; SM00406; IG
                                                                                                                                                                                subgroups.".
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                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                  DOMAIN
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                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                 HSSP; P80362;
                                                                                                                                          PIR; A01868; K1HUHU.
                                                                                                                                                                                                                     MEDLINE=71032830;
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-I REGION HAU
                                                                                   Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                        Hilschmann N.;
structure of a monoclonal kappa-type immunoglobulin
group I (Bence-Jones Protein Hau): subdivision withir
 .0895532
.089554
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                                                                                             IGV;
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01, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                                                     PubMed=4097974;
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72.0%;
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                                                                                                                                                            REGION OF THIS CHAIN HAS
                                                                                   Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                    A BENCE-JONES PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 408.5;
Pred. No. 2.7e
l2; Mismatches
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BY SIMILAR
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COMPLEMENTARITY-DETERMINING
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                                                                         FRAMEWORK 1.
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                  FRAMEWORK 4
                            COMPLEMENTARITY - DETERMINING
                                    COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                        FRAMEWORK
                                                                COMPLEMENTARITY-DETERMINING
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          SIMILARITY
                                                                                                                                                                       351:1291-1295(1970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody.
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Best Local (
                                                                   Matches
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DOMAIN 24 34
DOMAIN 35 49
DOMAIN 50 56
DOMAIN 57 88
DOMAIN 89 97
                                                                                                                         DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _HUMAN
                                                                                                                 SEQUENCE
                                                                                                                                                                                                                    InterPro; IPR003596; Pfam; PF00047; ig; 1 SMART; SM00406; IGV;
                                                                                                                                                                                                                                                         PIR; A01866; K1HUEU. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                        Biochemistry 9:3188-3196(1970).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARK-
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                           Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."; Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                          Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                       Intrachain disulfide bonds
                                                                                                                                                                                                                                                                                                            "The covalent structure of a human gamma G-immunoglobulin.
                                                                                                                                                                                                                                                                                                                                 MEDLINE=71064027; PubMed=4923144;
                                                                                                                                                                                                                                                                                                                                             DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=71064023; PubMed=5489770;
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
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                          1. DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS
                                            1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-I REGION EU.
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01, Last sequence update)
38, Last annotation updat
                                                                          70.7%;
70.1%;
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                                                                                                               11788 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                 16;
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                                                                         Score 397.5; DB 1 Pred. No. 3.9e-35;
                                                                           Pred.
                                                                                                                                                                               FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                  COMPLEMENTARITY-DETERMINING
                                                                                                                                                                     COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 402.5;
Pred. No. 1.
                                                                                                                                            FRAMEWORK
                                                                                                                                                            FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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DB 1;
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                                                                                 Length 108;
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"Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker."; J. Biochem. 77:1277-1296(1975).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN TREGION KA.
                                                                                                    MEDLINE=76189985; PubMed=818073;
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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HSSP; P80362; 1WTL.
                                                                                     Shinoda T
                                                                                                                                                                NCBI_TaxID=9606;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION BAN.
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DOMAIN 1 23 FRAN
DOMAIN 24 34 COM
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75; Conserv
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HSSP; P80362; 1WTL PIR; A01869; K1HUKA.

-! - MISCELLANEOUS: THIS

IS A BENCE-JONES PROTEIN.

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RESULT 15

KVIE_HUMAN

KVIE_HUMAN

AC

P01597;

DT

21-JUL-1986 (Rel. 01, Created)

DT

21-JUL-1986 (Rel. 01, Last sequence update)

DT

15-JUL-1998 (Rel. 38, Last annotation update)

DT

15-JUL-1999 (Rel. 38, Last annotation update)

DE

IG KAPPA CHAIN V-I REGION DEE.

OS

HOMO Sapiens (Human).

CE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominia

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominia

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Mammalia; Eutheria; Primates; Catarrhini; Hominia

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Mammalia; Eutheria; Primates; Catarrhini; Hominia

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro: IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
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DOMAIN
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amino acid sequence of a human kappa light chain.";
hem. J. 123:945-958(1971).
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BY SIMILARITY.
                                                                                                                       FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
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388.5; DB 1
No. 3.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473505 seqs, 146272329 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106
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230.521 Million cell updates/sec
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50.1 48.7	50.6	52.0	52.3	52.8	53.8	54.7	58.5	58.9	59.1	59.9	60.1	64.5	68.4	68.6	70.3	72.3	76.2	Query Match
97 109	101	114	238	106	99	107	109	109	109	108	298	107	214	108	107	108	108	Query Match Length
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Q9JL76 Q9N0W5	Q9JL78	Q9UL80	Q99M37	Q9U410	Q9JL74	Q9ERZ9	Q9UL86	Q9UL78	Q9UL85	Q9UL83	Q9QYF0	Q9JL84	Q9R1A5	Q9UL79	Q9UL81	Q9UL70	Q9UL77	ID
Q9j176 mus musculı Q9n0w5 oryctolagus	mus	Q9u180 homo sapien	Q99m37 mus musculu	Q9u410 schistosoma	Q9j174 mus musculu	Q9erz9 mus musculu	Q9u186 homo sapien	_	homo	OMO	Q9qyf0 mus musculu	Q9j184 mus musculu	mus	Q9u179 homo sapien	homo	homo	homo	Description

## ALIGNMENTS

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RESULT
Q9UL77
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                                                                                         Query Match 76.2%; Score 428.5; DB 4; Length 108; Best Local Similarity 76.6%; Pred. No. 3.3e-40; Matches 82; Conservative 8; Mismatches 16; Indels 1;
                                                                                                                                                                                                             EMBL; AF035037; AAD56273.1; -. HSSP; P01607; IREI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. NON_TER
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Q9UL77;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
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                                               DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                DIQMTQSPSSLSASVGDRYTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                           108 AA; 11738 MW;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    EMBL; AF035033; AAD56269.1;
                                                                                       Wu X., Liu B., Van Young D.C.;
                                                                                                                MEDLINE=98277139; PubMed=9614934;
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                     Q9UL81
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-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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MEDLLNE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                -!- SIMILARITY:
                                                                       "Myosin-reactive autoantibodies in rheumatic carditis
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108 AA;
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                                             87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 406.5; DB 4
Pred. No. 9.3e-38;
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Q9R1A5;
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NON_TER
SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                    Interpro; IPR003006; Ig_MHC
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UL79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK
                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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s; Pred. No. 1.7e-36;
10; Mismatches 20;
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                                                                                                                                                                                                        Score 385.5;
Pred. No. 2e-
             PRT;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REG
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                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                            acetyl-glucosamine antibodies from mice with autoimmune myocarditis.", Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C;
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SMART; SM00410; IG_like; 1.
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                                                                                                             RESGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK
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CE 298 F
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         (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
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                                                       PRELIMINARY;
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EMBLIEL. 17, Last annotation update)
IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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31867
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                                                                                                                                                                                                            Score 337.5;
Pred. No. 1.
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Pred. No. 7.
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1.4e-29;
hes 24;
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01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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MEDLINE=98277139; PubMed=9614934;
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SMART; SM00406; IGv; 1.
                                                                                                     SEQUENCE
                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; C
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR H
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                                                                                                                                                                                                                                                                                                                   AF035029; AAD56265.1;
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60.2%;
59.1%;
61.5%;
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Pred. No. 5.6e-30;
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Score 332; DB 4;
Pred. No. 1.8e-29;
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                     Length 109;
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                            O9UL86,
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              NCBI_TaxID=9606;
                                                                                                      Homo sapiens (Human)
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SMART; SM00406; IGV; 1.
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                   60 SRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                  61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                         11
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                                                                                                                                                                                                                                                                                                                           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                       1 DIOMTOSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGTEFTLTISSLQSEDFAITHCQQY-NSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003006;
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  58.9%;
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 P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                Score 331; DB 4;
Pred. No. 2.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87:184-192(1998)
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Kalis N.N.,
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 Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                              Length 109;
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RESULT
Q9ERZ9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406 IGv; 1.
NON_TER 107 107
SEQUENCE 107 AA; 1178
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

"Cloning and sequencing of the light chain fragment of variable genes of an anti-hTNF-a monoclonal antibody.";

- ^^11 Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L.,
Submitted (MAY-2000) to the EME
                                                                                                                                                                                                                          Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., "Construction and sequencing of the single-chain human TNF-alpha specific monoclonal antibody."; Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ERZ9;
                                                                                                                                            EMBL; AF262753; AAG23804.1;
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                        InterPro;
                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IFR003596; Ig_v.
InterPro; IFR003596; Ig_v.
Pfam; PF000407; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young D.C.; myosin-reactive autoantibodies in rheumatic carditis and
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                                                                                                                                                                    SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRFSGSGSRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF035028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. Immunopathol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                         IPR003599; Ig.
IPR003006; Ig_MHC
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                 11784 MW;
    54.7%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                            L., Han H., Yao L.B., EMBL/GenBank/DDBJ da
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 329; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                    AND
307.5; DB 1
No. 9.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
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                                                                                                                                                                    MAJOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
             DB 11;
                                                                                                                                                                 3J databases.
HISTOCOMPATIBILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                  Su C.Z.; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109
                                                                                                                                                                                        Su C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                    (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                Murinae; Mus
                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                COMPLEX
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Q9JL74
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Best Local
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                                                                                                                                                                                                    01-MAY-2000 (TrEMBLTel. 13, Last sequenc 01-JUN-2001 (TrEMBLTel. 17, Last annotat MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 VARIABLE REGION (FRAGMENT).
    Song X.T., Feng "Amplification,
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                   Schistosoma japonicum (Blood fluke).
                                                                                                                                                                                                                                                                                                         Q9U410;
01-MAY-2000 (TrEMBLrel.
                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
                                                                                                                                                                                                                                                                                                                                                             Q9U410
                                                                                                NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malkiel S., Liao L., Cunningham M.W., Diamond B., "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.", Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1999) to -i- SIMILARITY: TO IMMUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel 15, Created)
01-OCT-2000 (TrEMBLrel 15, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JL74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JL74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFSGSGSGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 YTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF206032; AAF69330.1;
Pro; IPR003006; Ig_MHC
Pro; IPR003596; Ig_v.
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                        Li Y.Q.,
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hes 23;
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Huang H.L.,
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Job time: 628 sec
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Best Local Similarity 54.8%
Matches 57; Conservative
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:5947).
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
NOW TER
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF207620; AAF19434.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-----NKYMAWYQQTPGKAPRLLIHYTSALQ 55
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                                                                     56; Conservative 22; Mismatches
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106 AA; 11478 MW; F20F544426BAE63E CRC64;
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